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Result
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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US-09-252-991A-27919
US-09-328-352-6329
US-09-328-352-6798
US-09-328-352-6798
US-09-252-991A-18872
US-08-665-259-27
US-08-762-500-27
US-08-711-731A-209
US-09-252-991A-21751
US-09-128-452A-242
US-09-252-991A-26621
US-09-128-452A-248
US-09-252-991A-26621
US-09-138-4500
US-08-97-080-89
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US-09-767-594-1
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Best Local S
Matches 187
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APPLICANT: Doyle, L. Austin
APPLICANT: Abruzzo, Lynne V.
APPLICANT: Abruzzo, Lynne V.
APPLICANT: Abruzzo, Lynne V.
APPLICANT: Abruzzo, Lynne V.
APPLICANT: FITTLE OF INVENTION: Breast Cancer Resistance Profittle Reference: Ross Unb conversion
CURRENT APPLICATION NUMBER: US/09/245,808
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/073763
EARLIER FILING DATE: 1998-02-05
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7 ; SEQ ID NO 1 ; LENGTH: 655 ; TYPE: PRT ; ORGANISM: Human N Sequence 1, Applicati Patent No. 6313277 GENERAL INFORMATION: SOFTWARE: Patentin 138 PSSPQLVRKC-VAHVRQHNQLLPNLTVRETLAFIAOMRLPRTFSQAQRDKRVEDVIAELR 196 79 SCQNSCELGI-QNLSFKVRSGQMLAIIGSSGCGRASENDVITGRGHGGKIKSGQIWINGQ 16 NTNG-----FPATASNDLKAFTEGA--VLSFHNICYRVKLKSGF------LP----19 DTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLASQVPWFEQLAQFKMPWTSP Similarity -CRKPVEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGL-SGDVLINGA PADFFLDIINGDSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYK-ETKAE PADFYVDLTSIDRR----SREQELATRE--KAQSLAALFLEKVRDL--DDFLWKAETK--RMSKQGRTIIFSIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNN RLAKGNRLYLISLHQPRSDIFRLFDLYLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSN LDKVADSKVGTQFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLK PRPANE -- KONSGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELG Application US/09245808 Conservative MCF-7/AdrVp cells Ver. 18.3%; Score 640.5; DB-4; 27.2%; Pred. No. 3.1e-62; 170. Mismatches 273; ALIGNMENTS Protein (BCRP) and Length 655; Indels ; 68 DNA which Gaps 229 256 78 169

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                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Homo sapiens; FEATURE: OTHER INFORMATION: human mitoxanthrone resistance (MXR)/BRCP/ABCP; OTHER INFORMATION: protein US-09-767-594-1
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Best Local Similarity
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PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Datanton
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CURRENT FILING DATE: 2001-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives FILE REFERENCE: 015280-402100US
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          231
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                     LAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNP 317
                                                                                  ROCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSR 257
                                                                                                                                                           SSPQLVRKC-VAHVRQHNQLLPNLTVRETLAFTAQMRLPRTFSQAQRDKRVEDVIAELRL 197
   MSKQGRTIIFSIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNP
                                                                                                                                                                                             CRKPVEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGL-SGDVLINGAP
                                                                 DKVADSKVGTQFIRGVSGGERKRTSIGMELITDPSILSLDEPTTGLDSSTANAVLLLLKR
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                           18.2%; Score 638.5; DB 4; 27.9%; Pred. No. 5.2e-62; tive 131; Mismatches 254;
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                                                            TELEFAX: (508) 872-541
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
MOLECULE TYPE:
                                                                                                           TELEPHONE: (508) 872-8400
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Dugan, Deborah A.
                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                TOPOLOGY:
                                                                                                                                          NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG
                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 17-JUN-1996
                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts
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                                             1684 amino
                                                                                                                                                                                                                                                                                                                                                                                                                   One Mountain Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burn, Timothy C.
Connors, Timothy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dackowski, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENZYME CORPORATION
                                                                                          872-5415
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JS-08-665-259-25
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APPLICANT: Van Raay, Terence J.
APPLICANT: Kiinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 ADFYVDLTSIDRR----SREQELATRE--KAQSLAALFLEKVRDL--DDFLWKAETK---
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Patent No. 603080
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Best Local Similarity
Matches 124; Conser-
                                                                                                                                                                                                                                                                                                                                                                                                                      ENERAL INFORMATION:
                                                               SOFTWARE: Patentin Rel
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
      APPLICATION NUMBER:
FILING DATE: 09-DEC-
CLASSIFICATION: 435
RIOR APPLICATION DATA:
                                                                                                                                                               ZIP: 01701
                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                              CITY: Framingham
                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08762500
                                                                                                                                                                                                                             One Mountain
                                                                                                                                                                                                                                                     Van Raay, Terence W.
Kilnger, Katherine W.
VENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
VENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
                                                                                                                                                                                                                                                                                                                                                  Landes, Gregory M.
Burn, Timothy C.
Connors, Timothy D.
Dackowski, William R.
                                                                                                                                                                               United States of America
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ilarity 24.8%;
Conservative 85
                                                                               PatentIn Release #1.0, Version
                        09-DEC-1996
N: 435
                                                  US/08/762,500
                                                                                                                                                                                                                             Road
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                                                                                                                          Sequence 75, Application US/08762500 Patent No. 6030806
                                                                                                           GENERAL INFORMATION:
                                                                          APPLICANT:
                                             APPLICANT:
                                                             APPLICANT:
                                APPLICANT:
TITLE OF INVENTION:
                 APPLICANT:
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US-08-762-500-25
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: IG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DALE.

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10469

APPLICATE: 17-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dugan, Deborah A. REGISTRATION NUMBER: 37,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
969 ALQAEGQEP---REVLGDLEE 986
                                                                                                                                                                            861 SDGIGALIEEERTAVKLNTGLALHCQQFWAMFLKKAAYSWREWKMV---AAQVLVPLTCV
                                                                                                                                                                                                                                                                                                                                                                     745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 KGNRLVLISLH-QPRSDIFRLEDLVLLMTS-----GTPIYL----GAAQHMVQYFTAIG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580 DMVQIRKSLGLCPQHDILFDNLTVAEHLYFYAQLK-----GLSRQKCPEEVKQMLHIIG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 QLV--RKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 NKDRAAVRDLNLNLYEGQITVLLGHNGAGKTTTLSMLTGL---FPPTSGRAYISGYEISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 NSCELGIQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSSP
                                                                                                                                                                                                                                                                                                                                                            EP---HCNPEDISQLVHHHVPNATLE-SSAGAELSFILPRESTHRFEGLFAKLEKKQKEL
                                        GLYTTG--PYFFAKILGELPE 503
                                                                                     TLALLAINYSS---ELFDDPMLRLTLGEYGRTVVPFSVPGTSQLGQQLSE--
                                                                                                                               TIGFLYFGHGSIQLSFMDTAALLFMIG----ALIPFNVI-LDVISKCYSERAMLYYELED
                                                                                                                                                                                                                                   TKMPGAV-----
                                                                                                                                                                                                                                                                                                                   DDFLWKAETKDLDE-----DTCVESSVT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CADTRYGNMYVRGLSGGERRRYSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLA 259
                                                                                                                                                                                                                                                                                                                                                                                                           YPCPRYSNPADF-----YVDLTSIDRRSREQELA---TREKAQSLAALFL---EKVRDL 356
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Pred. No. 9.6e-18;
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Dackowski, William R. Van Raay, Terence J. Klinger, Katherine W. Burn, Timothy C. Connors, Timothy D.

NOVEL HUMAN CHROMOSOME 16 GENES

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Gregory M.

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Best Local Similarity
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LENGTH: 1704 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Dollars
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US96/10469 FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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Pred. No. 9.8e-18;
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                                                                                                                                                             FALEUR NO. THEORNATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONI
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
SEQ ID NO 27569
LENGTH: 330
                                                                                                                                                                                                                                                                                             Patent No. 6551795
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                                              PRIOR APPLICATION NUMBER: US 60/0/4,/00 PRIOR EILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: 1998-07-27
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                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 -- ARYPHOLSGGOCORVALARSLVTRPRLLLLDEPLSALDARIRKHLREQIRRIQQELGL 447
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMON.

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 9
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RESULT 8
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US-09-252-991A-27569
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SEQ ID NO 20719
LENGTH: 370
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Best Local :
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APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 230; DB 4; L
Local Similarity 27.4%; Pred. No. 1.2e-16;
Les 83; Conservative 55; Mismatches 121;
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                        197 VYVTHDQGEALALSHRIAVMNQGRVEQLDAPETI-----YSFPRSRFVADFIGQCNL 248
                                                                                                267 ISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADF----Y 321
                                                                                                                                                                                 137 GRMPTQLSGGQRQRVAIARALVNRPRLLLLDEPLSALDAKLREEMQIELINLQKDVGITF 196
                                                                                                                                                                                                                                                                                  207
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                                                                                                                                                                                                                                                                                                                                       85 PVHTVFQSYALFPHMSVAQNIAFPLKM---AGVAKSEIDARVEQALKDVRL---ADK--G 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |:| : :|: ::| ||||: :|| :: | : ||:| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 IQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSSPQLVR-K 146
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Similarity 27.5%; Pred. No. 4.3e-18;
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US-09-252-991A-18872
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SEQ ID NO 18872
LENGTH: 345
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Best Local :
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Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
              201
                                     262 NRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFY
                                                                               146
                                                                                                                                                                         142 QLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQCA
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                                                                                                                                                                                                             31 LQPTRLNIQAGQIFGLIGHSGAGKSTLLRLI---NRLEEPSGGRILVEGEDVTALDAEGL
                                                                                                                                                                                                                                            88 IQNLSFKVRSGOMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSSP-----
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                                                                                                 DTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKG
                                                                                                                                            RRFRQRVGMIFQHFNLLSSKTVADNIAM--PLRLAGGFSRAEVDARVSELLARVGLSDHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFRPEAVELVDDFGSDKESLYL-----PVKVLSTEFLGAKRRLFCAIHIDGIEQAKH 394
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       LKLTIVLITHEMDVIRRVCDQVAVMDGGAIVEQGDVADVFLH----
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US-08-665-259-27
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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TOPOLOGY: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dugan, Deborah A. REGISTRATION NUMBER: 37,315
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                    141 PQL--VRKCVAHVROHNQLLPNLTVRETLAFIAOMRLPRTFSQAQRDKRVEDVIAELRLR 198
                                                                                                                                                                                                                                        22 KNDKKLALNKLSLNLYENQVVSFLGHNGAGKTTTMSILTGL---FPPTSGSATIYGHDIR 78
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                                KPGRTILLSTHHMDEADL--LGDRIAIISHGKLKCCGSPLFLKGAYXDGYRLTLVKQPAE
                                                                  AKGNRLYLISLHQPRSDIFRLFDLYLLMT-----SGTPIYLGAAQHMVQYFTAIGYP--
                                                                                                                                     QCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRL
                                                                                                                                                                       TEMDEIRKNLGMCPQHNVLFDRLTVEEHLWFYSRL---KSMAQEEIRKETDKMIEDLEL-
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                                                                                                     --SNKRHSLVQTLSGGMKRKLSVAIAFVGGSRAIILDEPTAGVDPYARRAIWDLILKY
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Klinger, Katherine W.

Klinger, Katherine W.

VENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

VENTION: COMPOSITIONS, METHODS OF MAKING
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Best Local Similarity
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                                                                                                                                                                                                                                                                       MOLECULE TYPE: -762-500-27
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                                                                                                                                                                                                                                                                                                                                                                                                                     ELECOMMUNICATION INFORMATION: TELEPHONE: (508) 872-8400
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                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
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        QCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRL 258
                                                                                         PQL--VRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLR 198
                                                                                                                          KNDKKLALNKLSLNLYENQVVSFLGHNGAGKTTTMSILTGL---FPPTSGSATIYGHDIR 78
                                                                                                                                                        QNSCELGIQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSS 140
                                                                                                                                                                                                                                                                                                                                    amino acid
                                                        TEMDETRKNLGMCPQHNVLFDRLTVEEHLWFYSRL---KSMAQEETRKETDKMIEDLEL- 134
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                                                                                                                                                                                                                                                                                                      unknown
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Burn, Timothy C.
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Patent No.
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Best Local
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ORIGINAL SOURCE:
ORGANISM: MYC
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                    147 CVAHVRQHNQLLPNLTVRETLAF---IAQMRLPRTFSQAQRDKRVEDVIAELRLRQCADT 203
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                                                                                                  24 VHDLSITVADGEFLILIGPSGCGKTTTLNMIAGL---EDISSGELRIDGDRVNEKAPKDR
                                                                                                                                88 IQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSSPQLVR-K 146
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RVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNR 263
                                 DIAMVFQSYALYPHWTVRQNIAFPLMLAKVK-----KAEIAQKVSETAQILDLTDLLDR 134
                                                                                                                                                                                                                                                                                                                                             amino acid
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RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/311,731A
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Pred. No. 2e
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US-09-252-991A-21751
: Sequence 21751, Application US/09252991A
: Patent No. 6551795
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SEQ ID NO 21751

LENGTH: 676

TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
S-09-252-991A-21751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: MARC J. Rubenfield et al.
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LE REFERENCE:
                                                                           485 DQIEAMTLGDKVAV-MKDGVIQQF---GTPQQIYNDPANLFV 522
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                                                                                                                    281 DLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYV 322
                                                                                                                                                              436 MGRALARRPKVYLFDEPLSNLD------AKLRVEMRTELKLMHQRLKTTTVYVTH 484
                                                                                                                                                                                           223 IGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRLVLISLHQ--PRSDIFRLF 280
                                                                                                                                                                                                                                                  384 VRENIAFGLKI---RKMPQAAIDEEVARVARLLQIEHLLERKPSQ-----LSGGQQQRVA 435
                                                                                                                                                                                                                                                                                              163 VRETLAFIAOMRLPRTFSQAORDKRVEDVIAELRLRQCADTRVGNMYVRGLSGGERRRVS 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 TLEVRDL--NYQVDLASQVPWFEQLAQFKMPWTSPSCQNSCELGIQNLSFKVRSGQMLAI 103
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Post processing: Minimum Match 0%
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Listing first 45 summaries
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Talieuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ver. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10817197
A;Accession: C84423
A;Status: preliminary
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84423
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A; Residues: 1-725 <STO>
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401 AWMQASRDGPTNKVRARMSVASAVIFGSVFWRMGKSQTSIQDRMGLL-QVAAI---NTAM
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                                                                                                                                                                                                                                                                                                72 WRNITCSLSDKSSKSVRFLLKNVSGEAKPGRLLAIMGPSGSGKTTLLNVLAGQLSLSPRL
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                        QISNDFRDLPTLLIHGAEACLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVIL
                                               ------SSSVLYATPLS---MKEETKNGMRPRRKAIVERTDGWWRQFFLLLKR
                                                                         KAETKDLDEDTCVESSV---TPLDTNCLPSPTK-----
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Result

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735.5 723.5 720 668.5 656 653 651.5 651.5 651.5 591 591 599.5 599.

Database

Maximum Minimum

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seq

Title: Perfect score:

Scoring table: Sequence:

Searched:

Run

OM protein

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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712

A; Status: preliminary
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
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C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Residues: 1-646 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                  370
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                                                                                                                                                                                                                                                                                                                                                                                                                     72 WKSKE----KTILNGITGMVCPGEFLAMLGPSGSGKTTLLSALGGR--LSKTFSGKVMY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 GLODRLFSSESDNSLYF-TYSGQPN-----TLEVRDLNYQVDLASQVPWFEQLAQFKMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                               LRURQCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WTSPSCONSCELGIONLSFKVRSGOMLAIIGSSGCGRASLLDVITGRGHGGKIKSGOIWI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLPD-MSDTQSKSVLAFPTITSQPGLQMSMYPITLKEVVYKVKI------EQTSQCMGS 71
                                                                                                                                              IKRLASGGRTVVTTIHQPSSRIYHMFDKVVLLSEGSPIYYGAASSAVEYFSSLGFSTSLT
                                                                                                                                                                                                                                     LGLNRCINSMIGGPLFRGISGGEKKRVSIGQEMLINPSLLLLDEPISGLDSTTAHRIVTT
                                                                                                                                                                                                                                                                                                                                                     NGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAAQSRILMFWYSATYLLL 655
         EDTCVESS----VTPLDTNCLPSPTKMPGAVQQFTTLIRRQI-SNDFRDLPTLLIHGAEA
                                                      VNPADLLLDLANGIPPDTQKETSEQEQKTVK--ETLVSAYEKNI---
                                                                                              SNPADFYVDLTS----IDRRSREQELATREKAQSLAALFLEKVRDLDDFLWKAETKDLD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MELDSYPLY ---- AIYLIV 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGQPFSGCIKRR-TGFVAQDDVLYPHLTVWETLFFTALLRLPSSLTRDEKAEHVDRVIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt NTPIIFRWIPRASLIRWAFQGLCINEFSGLKFDHONTFDVQTGEQALERLSFGGRRIRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLWTVPAWISKVSFLRWCFEGLMKIQFS-----RRTYKMPLGNLT---IAVSGDKILSA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPTLSRFGKFCGIVTVESFAASAMGLTVGAMVPSTEAAMAVGPSLMTVFIVFGGYYVNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPGLQPFLLHFLLVWLVVFCCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLS 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AE005172; NID:g11136734; PIDN:AAG31315.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.6%; Score 723.5; DB 2
30.6%; Pred. No. 2.7e-49;
tive 119; Mismatches 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                      ----STK-LK 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E.; Kim, C
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Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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C; Superfamily: fruit fly white protein; ATP-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable ABC transporter F17M19.11 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cross) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Date: 03-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: E96742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
E96742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: F17M19.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-609 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
298 QHMVQYFTAIGYPCPRYSNPADFYVDLTSIDRRSREQELATREK---AQSLAALFLEKVR 354
                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                       119 TGRGHGGKIKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQWRLPRT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 CLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELED
                                                                                                                                                                                                                                                                                                                                         2 SNDSCNIKKLLGLKQKDSDETRSTEERTILSGVTGMISPGEFMAVLGPSGSGKSTLLNAV
                                                                                                                                                                               FSQAQRDKRVEDVIAELRLRQCADTRVGNMYVRGLSGGERRRVSIGVQLLMNPGILILDE 238
                                                                                                     PTSGLDSFTAHNLVKTLSRLAKG-NRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAA
                                                                                                                                                          LTRDVKLRAAESVISELGLTKCENTVVGNTFIRGISGGERKRVSIAHELLINPSLLVLDE
                                                                                                                                                                                                                                                 AGRLHGSNL-TGKILINDGKITKQTLKR-TGFVAQDDLLYPHLTVRETLVFVALLRLPRS
                                                                                                                                                                                                                                                                                                                                                                                      TSPSCQNSCELGI-QNLSFKVRS-------GQMLAIIGSSGCGRASLLDVI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLIVIGLSGGFMVLYYVSLR
                                                                  PTSGLDATAALRLVQTLAGLAHGKGKTVVTSIHQPSSRVFQMFDTVLLLSEGKCLFVGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLGIQYTDDDYYECSKGVWCRVGDFPAIKSMGLNNLWI----DVFVMGVMLVGYRLMA- 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGLAFGALLMNIKQATTLASYTTLYFLIAGGYYVQ-----QIPPFIVWLKYLSYSYYCYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVP---AWISKVSFLRWCFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0%; Score 700; DB 2;
9%; Pred. No. 1.9e-47;
103; Mismatches 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 609
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 122;
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QY 82 NSCELGIQN-LSFKVRSGQMLAIIGSSGCGRASLLDVITGRCHGGKIKSGQIWINGQPSS 140 161 SSSEKSILNGISGSAYPGELLALMGPSGSGKTTLLNALGGRENQQNI-GGSVSYNDKPYS 219 QY 141 PQLYRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQC 200 :	RESULT 4 746101 ABC transporter-like protein - Arabidopsis thaliana N;Alternate names: protein T25B15.80 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 C;Accession: T46101 R;Alternate number: 223021 A;Reference number: 223021 A;Reference number: 223021 A;Residues: preliminary A;Residues: 1-737 <alc> A;Cross-references: EMEL;AL132972 A;Cross-references: EMEL;AL132972 A;Cross-references: EMEL;AL132972 A;Experimental source: cultivar Columbia; BAC clone T25B15 C;Genetics: A;Map position: 3 A;Note: T25B15.80 Query Match Best Local Similarity 28.0%; Pred. No. 7.7e-45; Matches 189; Conservative 134; Mismatches 258; Indels 93; Gaps 16; Oy 25 DRLFSSESDNSLYFTYSGOPNTLEVRDLNYOVDLASQVPWFEQLAQFKMPWTSPSCQ 81 10 DILEDIEAATSSVVKFQAEPTFPIYLKFIDITYKVTTKGMT 160</alc>	Db 240 RDAMAYFESVGFSPAFPMNPADFILDIANGVCQTDGVTEREKDNVRQTLVTAY 292 Oy 355 DLDDFLWKAETKDLDEDTCVESSVTPLDTNCLPSPTKMPGAVQQFTTLI
A; Molecule type: DNA A; Molecule type: DNA A; Rosidues: 1-24, 'LIFEIPYHCRVTAD', 30-687 < COHA2> A; Cross-references: EMBL:X02974; NID:g10873; PIDN:CAA26716.1; PID:g10874 A; Cross-references: Extrain Canton S C; Genetics: A; Gene: white; w A; Gene: white; w A; Gene: white; w A; Cross-references: FlyBase:FBgn0003996 A; Introns: 24/3; 116/1; 334/2; 439/3; 483/3 C; Superfamily: fruit fly white protein; ATP-binding cassette homology C; Reywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein F; 133-1317/Domain: ATP-binding cassette homology <abc> F; 130-137/Region: nucleotide-binding motif B F; 67,93,472,554,651/Binding site: carbohydrate (Asn) (covalent) #status predicted Query Match Best Local Similarity 30.3%; Pred. No. 6.9e-44; Matches 178; Conservative 113; Mismatches 265; Indels 32; Gaps 10;</abc>	RESULT 5 FYFFW white protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 31-Dec-1990 #sequence_revision 17-Feb-1995 #text_change 19-Jan-2001 C;Accession: S08635; S07263; S10240 R;Pepling, M.; Mount, S.M. Nucleic Acids Res. 18, 1633, 1990 A;Title: Sequence of a CDNA from the Drosophila melanogaster white gene. A;Reference number: S08635; MUID:90221897; PMID:2109311: A;Accession: S08635 A;Molecule type: mRNA A;Residues: 1-887 <pep> A;Cross-references: EMBL:X51749; NID:98825; PIDN:CAA36038.1; PID:98826 A;Title: DNA sequence of the white locus of Drosophila melanogaster. A;Reference number: S07263; MUID:85134865; PMID:6084717 A;Accession: S07263 A;Molecule type: DNA A;Residues: 1-24, 'LIFEIPYHCRVTAD', 30-334, 'ITLHLNSYPAWVPSVLPTTIRRTFTYRCWPLCPDGRSSPN A;Cross-references: EMBL:X03974 A;Experimental source: strain Canton S R;O'Hare, K. Submitted to the EMBL Data Library, June 1985 A;Rocession: S10240 A;Accession: S10240</pep>	Db 399 LLDLVNGNNNDISVPSALKEKMKIIRLELVVRNVKCDVETQYLEEAYKTQIA 450 Qy 380 PLDTNCLPSPTKMPGAVQOFTTLIRRQISNDFRDLPTLLIHGAEACLMSH

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JC7860

brain multidrug resistance protein, BMDP - pig
C;Specles: Sus scrofa domestica (domestic pig)
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change
C;Accession: JC7860
R;Elsenblaetter, T.; Galla, H.J.
Biochem. Biophys. Res. Commun. 293, 1273-1278, 2002
A;Title: A new multidrug resistance protein at the blood-brain b.
A;Accession: JC7860; MUID:22050127; PMID:12054514
A;Accession: JC7860
                                                                                                                                                                                                                                            A;Cross-references: GB:AJ420927
A;Experimental source: brain
C;Comment: This protein, a new transport protein of the ATP-binding cassette (ABC) superexclusion of xenobiotics from the brain and participates in drug transport across the blC;Genetics:
A;Gene: bmdp
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                                         78 PSCQNSCELGI-QNLSFKVRSGQMLAIIGSSGCGRASLLDVITGR--GHGGKIKSGQIWI
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| GVPGRVKGLSGGERKRLAFASEALTDPPLLICDEPTSGLDSFTAHSVVQVLKKLSQKGKT
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                                                                                             RNTNGL----PGSSSNELKTSAGGA--VLSFHDICYRVKVKSGFLF----
                                                                                                                             QDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLASQVPWFEQLAQFKMPWTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCFEGLMKIQFS---RRTYKM
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                                                                                                                                                                  Score 653; DB 2;
Pred. No. 1.1e-43;
3; Mismatches 270;
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                                         A; Experimental source; strain S288C
A; Note: this sequence has been revised in reference S77690
A; Note: this was assumed to be the complete sequence of pr
                                    A; Note: this was assumed C; Genetics:
                                                                                                                          A; Molecule type: DNA
A; Residues: 200-1294 <ALF>
                                                                                                                                                                           A;Cross-references: EMBL:Z74816
A;Experimental source: strain S288C
A;Note: this sequence has been revised in reference S77690
A;Note: this was assumed to be protein YOL074c
                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1294 <ALE>
A;Cross-references: EMBL:Z74816; MIPS:YOL075c
A;Cross-thic is a revision to the sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
S77690
                 A;Cross-references: SGD:S0005435
                                                                                                        A; Cross-references: EMBL: Z74817
                                                                                                                                                                A; Accession: S66768
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A; Residues: 1-179, 'TTRTGVFLVVKRED'
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A; Accession: S77690
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                                               of protein YOL075c
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521 440 472 391

581

412

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352

286

226

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hypothetical protein F27G19.20 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 17-Mar-2000 C; Accession: T08934 R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, & submitted to the Protein Sequence Database, May 1999 A; Reference number: Z16519 A; Accession: T08934 A; Molecule type: DNA
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A; Note: YOL075c
C; Superfamily: u
C; Keywords: ATP;
F; 45-263/Domain:
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F;606-622/Domain:
F;710-916/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496-512/Domain: transmembrane #status predicted <TM3>
506-622/Domain: transmembrane #status predicted <TM4>
710-916/Domain: ATP-binding cassette homology <ABC2>
727-734/Region: nucleotide-binding motif A (P-loop)
1042-1058/Domain: transmembrane #status predicted <TM5>
11125-1141/Domain: transmembrane #status predicted <TM6>
1177-1193/Domain: transmembrane #status predicted <TM6>
1177-1193/Domain: transmembrane #status predicted <TM7>
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Matches 171;
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                                                                                                                                                                                                                                                                                                                603
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                                                                                                                                                                                                                                                                                                                                                                                      RIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQLQAESYI-SNATEIQIQNM--TTRLP-FWKQVTVLTRRNFKLNFSDYVTLISTFAEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVEQLIEELGLKDCADTLVGDNSHRGLSGGEKRRLSIGTQMISNPSIMFLDEPTTGLDAY 219
                                                                                                                                                                                                                                                                                                           LMKIQFSRR----TYKMPLGNLTIAVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGLYTTGPYFFA-KILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IIGTVCGWIYYKPDKSSIGGLRTTTACLYASTILQCYLYLLFDTYRLCEQDIALYDRERA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAHNLYKTLSRLAK-GNRLYLISLHQPRSDIFRLFDLYLLMTSGTPIYLGAAQHMYQYFT 305
                                                                                                                                                                                                                                                                                                                                                  SGLSMLSVAVSRDFSKASLVGNMTFTVLSMGCGFFVNAKVMPVYVRWIKYIAFTWYSFGT
                                                                                                                                                                                                                                                                                                                                                                                                                           EGSVTPLAFIVARKISLFLSDDFAMTMIFVSITYFMFGLEADARKFFYQFAVVFLCQLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDLDEDTCVESSVTPLDTNCLPSPTKMPGAVQQFTTLIRQISNDFRDLPTLLIHGAEAC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIGYPCPRYSNPADFYVDLTSIDRRSREQELATREKAQSLAALFLEKVRDLDDFLWKAET 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VEDVIAELRLRQCADTRYGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSF 246
                                                                                                                                                                                                                                                                     LMSSTFTNSYCTTDNLDECLGNQILEVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIP--FNVILDVISKCYSERAMLYYELE 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAFLVIKTLKKLAKEDGRTFIMSIHQPRSDILFLLDQVCILSKGNVVYCDKMDNTIPYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNTFSMDLPSGSVMAVMGGSGSGKTTLLNVLASKISGGLTHNGSIRYVLEDTGSEPNETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKRAHLDGQ-DHPIQKHVIMAYLPQQDVLSPRLTCRETLKFAADLKL----NSSERTKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---WINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane #status predicted <TM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 653; DB 2;
Pred. No. 2.9e-43;
1; Mismatches 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #status predicted
                                                                                                                                                                                                                                                                     595
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                                                                             Bancroft
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A; Molecule type: mRNA A; Residues: 1-638 < CR

<CRO>

EMBL: U34919;

NID:g1314276; PIDN:AAC51098.1;

PID:g1314277

C; Genetics: A;Cross-references: A; Reference number: H00769 A; Accession: G02068

A; Status: preliminary; translated

from GB/EMBL/DDBJ

R;Croop, J.M.; Tiller, G.; Fletcher, J.A.; submitted to the EMBL Data Library, August

August

Lux, 1995

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Raab,

E9 ...

Goldenson, D.;

Arcin

C; Accession: G02068

white homolog -

G02068

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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 02-Feb-2001

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A,Map position: 4
A,Map position: 4
A;Introns: 38/3; 253/1; 304/1; 414/3
A;Introns: 38/3; 253/1; 304/1; 414/3
C:Snberfamily: fruit fly white protein; ATP-binding cassette homology
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A;Cross-references: EMBL:AL078467; GSPDB:GN00062; ATSP:F27G19.20
A;Experimental source: cultivar Columbia; BAC clone F27G19
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: ATSP: F27G19.20
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Best Local Similarity
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GYYTYKLLILGQYT 573
                                   SRRTYK-MPLGNLT 621
                                                                  LGALVMDQKSATTLGSVIMLTFLLAGGYYVQ-----HVPVFISWIKY--
                                                                                                                                        LSPYFLSRVVGDLPMELILPTCFLVITYWMAGLNHNLANFFVTLLVLLVHVLVSGGLGLA
                                                                                                                                                                           TGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALA 548
                                                                                                                                                                                                               LCGLLWW----QTKISRLQDQIGLLFFISSFWAFFPLFQQIFTFPQERAMLQKERSSGMYR
                                                                                                                                                                                                                                                                                                                                                             ANGKPLLVISCWPSVGSDESQRPEAMKAALVAFYKTNLLDSVINEVKGQD----DLCNKPR
                                                                                                    AAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCFEGLMKIQF 608
                                                                                                                                                                                                                                                 TIGFLYFGHGSIQLS-FMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELEDGLYT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTTIHQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILKGLTGIVKPGEILAMLGPSGSGKTSLLTALGGRVGEGKGKLTGNISYNNKPLS-KAVK
                                                                                                                                                                                                                                                                                     ESS--RVATNTYGDWPTTW---WQQFCVLLKRGLKQRRHDSFSGMKV----AQIFIVSF
                                                                                                                                                                                                                                                                                                                       ESSVTPLDTNCLPS-PTKMPGAVQQFTTLIRRQIS----NDFRDLPTLLIHGAEACLMSM 429
                                                                                                                                                                                                                                                                                                                                                                                                 TSIDR------RSREQELATREKAQSLAALFLEKVRDLDDFLWKAETKDLDEDTC---V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPFLRGVSGGERKRVSIGQEILINPSLLFLDEPTSGLDSTTAQRIVSILWELARGGRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTTGFVTQDDALYPNLTVTETLVFTALLRLPNSFKKQEKIKQAKAVMTELGLDRCKDTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SESDNSLYFTY---SGQPNTLEVRDLNYQVDLASQVPWFEQLAQFKMPWTSPSCQNSCEL
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31.1%;
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4; Mismatches
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Pred. No. 1.4
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RESULT 10
D96553
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Nature 408, 816-820, 2000
A;Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Falzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
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C;Superfamily: f:
C;Reywords: ATP;
F;61-253/Domain:
F;78-85/Region: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     FLRWCFEGLMKIQF--SRRTYKMPLGNLTIAVSGDKILSAMELDSYPLYAIYLIVIGLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTIHQPSAKLFELFDQLYVLSQGQCVYRGKVCNLVPYLRDLGLNCPTYHNPADFVMEVAS
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                                                                                                                                                                                                                                                                                             GFMVLYYVSLRFI
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                                                                                                                                                                                                                                                                                                                                                                                                                      VWLVVFCCRIMALAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGVFLREHLNYWYSLKAYYLAKTMADVPFQIMFPVAYCSIVYWMTSQPSDAVAFVLFAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGL-----YTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGLLYLGIGNEAKKVLSNSGFLFFSMLFLMFAALMP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDSSSMEGCHSFSASCL------TQFCILFKRTFLSIMRDSVLTHLRITSHIGIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQCADTRVG
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                                                                                                                                                                                                                                                             ----IFFISLRLI
                                                                                                                                                                                                                                                                                                                           YVRYGFEGVILSIYGLDREDLHCDIDETCHFQKSEAILRELDVENAKLY-LDFIVLG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDRRSREQEL--ATREKAQSLAALFLEKVRDL-----DDFLWKAET------KDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ~LKGISGKFNSGELVAIMGPSGAGKSTLMNILAGYRETG--MKGAVLINGLPRDLRCFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNNLTEAQRESSLPRRAAVNIEERDLSYSV---PEGPWWRKKGYKTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNSLYFT--YSGQPN----TLEVRDLNYQVDLASQVPWFEQLAQFKMPWTSPSCQNSCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative · 130;
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25.7%;
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Pred. No. 6.5e-41;
0; Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GMCDSDHKRDLGGDAEVNPFLWHRPSEEVKQTKRLKGLR
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                                                                                                A.R.; Creasy, T.H.;
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                               Khaykin, E.; Kim,
Maiti, R.; Marzia
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C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette
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A;Title: Sequence and analysis of chromosome 1 of the plant
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96553
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A; Residues: 1-687 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB: AE005173; NID: g10092349; PIDN: AAG12758.1;
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VLILV----CYRILFFIVLKLKERAEPALKAIQAKRTMKSLKKRPS
                                 YLIVIGLSGGFMVLYYVSLRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISLHQPRSDIFRLEDLYLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDLTS
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                                                           ISFMSYGSWAIQGAYKNDFLGLEFD-PMFAGEPKMTGEQVINKIFGVQVTHSKWWDLSAI
                                                                                          ISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVSGDKILSAM-----ELDSYPLYAI
                                                                                                                        NIFFSVSVIESLMMVVASLVPNFLMGLITGAGIIGIIMMTSGFFRLLPDLPKVFWRYP--
                                                                                                                                                       LVWLVVFCCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSL----WTVPAW
                                                                                                                                                                                    EMKVFYKERLSGYYGVSVYIISNYVSSFPFLVAIALITGSITYNMVKFRPGVSHWAFFCL
                                                                                                                                                                                                               ERAMLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFL
                                                                                                                                                                                                                                                VIY----IVVSFCVGTIFYDVGH-----SYTSILARVSCGGFITGFMTFMSIGGFPSFIE
                                                                                                                                                                                                                                                                             LIHGAEACLMSMTIGFLYF--GHGSIQLSFMDTAALLFMIGALIPFNVILDV--ISKCYS
                                                                                                                                                                                                                                                                                                                                             TCVE---
                                                                                                                                                                                                                                                                                                                                                                     SDFDTVTATLKGSQRIRETP-ATSDPLMNLATSEI-KARLVENYRRSVYAKSAKSRIREL
                                                                                                                                                                                                                                                                                                                                                                                                    ID-----RRSREQELATREKAQSLAALFLEKVRDLDDF----LWKAETKDLDED
                                                                                                                                                                                                                                                                                                                                                                                                                                   SSIHOPSSEVFALFDDLFLLSSGETVYFGESKFAVEFFAEAGFPCPKKRNPSDHFLRCIN
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26.9%;
                                                                                                                                                                                                                                                                                                                                        -SSVTPLDTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDL----PTL
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Pred. No. 4.
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.9e-39;
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                              - IKQKPS
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RESULT T47652 11

ABC transporter-like protein - Arabidopsis thaliana
N;Alternate names: protein T26112.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
C;Accession: T47652
R;Monfort, A; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; M submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24471
A;Accession: T47652 K.; Mayer,

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protein C05D10.3 [imported] - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 10-May-2001 #sequence_revision 10-May-2001 #1 C:Accession: 884474 R:anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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A;Experimental source: cultivar Columbia; BAC C;Genetics:
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A;Residues: 1-725 <MON>
A;Cross-references: EMB
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           Reference
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           number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                               PTFHMASFFSNALYNSFYLAGGFMINLSSL---WTVPAWISKVSFLRWCFEGLMKIQFS-
                                                                                                                                                                                                                                                                                                                                                                                                            FAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALAAAALL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGHGSIQLSFMDTAALLFMIGALIP--FNVILDVISKCYSERAMLYYELEDGLYTTGPYF 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCLPSPTKM-----
                                                                                                                                                                                                                            YPLYAIYLIVIGLSGEMVLYYVSLRF
                                                                                                                                                                                                                                                     PSRCFVRGVQVFDSTLLGGVSDSGKVKLLETLSKSLRTKITESTCLRTGSDLLAQQGITQ
                                                                                                                                                                                                                                                                                                                  PNIMLCYMVSITYLAYCLLLSGFYVNRDRIPFYWT---WFHYISILKYPYEAVLINEFDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSRSNPTSMETVSSYANPSLFETF-ILAKRYMKNWIR-MPELV--GTRIATVMVTGCLLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSLAALFLEKVRDLDDFLWK------AETKDLDED-----TCVESSVTP---LDT 383
                                                                                                                                                                                                                                                                                                                                                                               ISHSLVSLPQLLAPSLVFSAITFWTVGLSGGLEGEVFYCLLIYASFWSGSSVVTFISGVV
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                                                                                                                                                                                              LSKWDCLWITFASGLFFRILFYFALLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGIDIIHDPIVLFLDEPTSGLDSTNAFMVVQVLKRIAQSGSIVIMSIHQPSARIVELLDR
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         sequence of
ber: A75000;
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25.5%;
    the nematode C. elegans: a MUID:99069613; PMID:9851916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PGAVQQFTTLIRRQISNDFRDLPTLLIHGAEACLMSMTIGFLY 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 591; DB 2; I
Pred. No. 1.1e-38;
5; Mismatches 273;
                                                                                10-May-2001 #text_change
                                                                                                                                                                                              718
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                 investigating
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                                                                                                               RESULT 13
747648
747648
ABC transporter-like protein - Arabidopsis thaliana
N;Alternate names: protein T15C9.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000
C;Accession: T47648
         A; Molecule type: DNA
A; Molecule type: DNA
* Dosidues: 1-720 <MEW>
A;Residues: 1-720 < A;Cross-references:
                                                              A; Reference number: Z24470
A; Accession: T47648
                                                                                           submitted to the Protein
                                                                                                        R; Mewes, H.W.; Rudd, S.;
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                                           Status: preliminary
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EMBL: AL132970

Lemcke, Sequence

χ : K.; Mayer, Database,

April 2000 K.F.X

#text_change

19-May-2000

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A; Residues: 1-559 <STO>
A; Cross-references: GB:
A; Note: similar to D. mo
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A; Status: preliminary
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A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 199
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Best Local Similarity
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522
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                                                                                                                                                                LEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFC
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                                  E,
                                                               AISISYAVATIFANTDVAMTILPIFVVPIMAFGGFFITFDAIPSYFKWLSSLSYFKYGYE
                                                                                              CRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCFE
                                                                                                                               NANGYYRTSAYFLAKNIAELPQYIILPILYNTIVYWMSGLYPNFWNYCFASLVTILITNV
                                                                                                                                                                                                                                       TIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDV-----ISKCYSERAMLYYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAHVRQHNQLLPNLTVRETLAFIAQMRL-PRTFSQAQRDKRVEDVIAELRLRQCADTRVG
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523
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D. melanogaster white protein
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29.3%; Pred. No. 9.16
tive 98; Mismatches
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A; Experimental source: c
C; Genetics:
A; Map position: 3
A; Note: T15C9.80
C; Superfamily: Arabidops
A:Reference number: Z24470
A:Accession: T47650
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-708 <MEW>
                                                                                           N; Alternate names: protein T15C9.110 C; Species: Arabidopsis thaliana (mouse C; Date: 20-Apr-2000 #sequence_revision C; Accession: T47650
                                                               R; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Da
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;Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein
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                                                                                                                                                transporter-like protein - Arabidopsis thaliana
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                                                                                                                                                                                                                 LKQQGVTQLSKWNCLLITVGFGFLFRILFYLCL 7.11
                                                                                                                                                                                                                                           LSAMELDSYPLYAIYLIVIGLSGGFMVLYYVSL 662
                                                                                                                                                                                                                                                                   VLQNEFSDPTECFVRGVQLFDNSPLGELTYGMKLRLLDSVSRSIGMRISSSTCLTTGADV
                                                                                                                                                                                                                                                                                              LMKIQFSRRTY------KMPLGNLTIAV-----
                                                                                                                                                                                                                                                                                                                        SSFVTFLSGVVPHVMLGYTIVVAILAYFLLFSGFFINRDRIPQYWIWFHYLSLVKYPYEA
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                                                                                                    (mouse-ear cress)
evision 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 589.5; DB 2; Pred. No. 1.4e-38;
                                                                  Database,
                                                                             Mayer,
                                                                             K.F.X.
                                                                April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EAISASISRGKLVSGGGGGSSVI 396
                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FYTCADALPVFLQERYIFMRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289;
                                                                                                       #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 720;
                                                                                                     19-May-2000
                                                                                                                                                                                                                                                                                              SGDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -IDRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F12L6.1;
                                                                                                                                                                                                                                                                                              629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452
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A; Map position: 3
A; Note: T15C9.110
C; Superfamily: Arai
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A;Experimental source: cultivar Columbia;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 IGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQP-SSPQLVRKCVAHVRQHNQLLPNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAVLINEFDDPSRCFVKGVQVFDGTLLAEVSHVMKVKLLDTLSGSLGTKITESTCLRTG
                                                                                           FEGLMKIQF---SR---RTYKMPLGNLTIAVS-----
                                                                                                                                     WSGSSIVTFISGLIPNVMMSYMVTIAYLSYCLLLGGFYINRDRIPLYWIWFHYISLLKYP
                                                                                                                                                                                                                                      RETTHNAYRTSSYVISHALVSLPQLLALSIAFAATTFWTVGLSGGLESFFYYCLIIYAAF
                                                                                                                                                                                                                                                                                YELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVV
                                                                                                                                                                                                                                                                                                                                                                                                                           SMETVSSYANPP--LAETFILAKRYIKNWIRTPELIGMRIGTVMVTG----LLLATVYWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTNCLPSPTKMPGAYQQFTTLIRRQISNDFRD-----LPTLLIHGAEACLMSMTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIILSHGKSVFNGSPVSLPSFFSSFGRPIPEKENITEFALDVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDLTSIDRRSREQELATREKA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQCADTRVGNMYVRGLSGGERRRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGGSGAGKSTLIDALAGRVAEDSLK-GTVTLNGEKVLQSRLLKVISAYVMQDDLLFPMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNTLEVRDLNYQVDLASQVPWFEQLAQFKMPWTSPSCONSCELGIQNLSFKVRSGQMLAI
                                                                                                                                                                                       FCCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSLAALFLEKVRDLDDF--LW-----KAETK---DLDEDTCV------ESSVTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRLVLISLHQPRSDIFRLFDL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFLLSFNNLSYNVVLRRRF------DFSRRKTA-----SVKTLLDDITGEARDGEILAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGIDITHDPILLFLDEPTSGLDSTNAFMVVQVLKRIAQSGSVVIMSIHQPSARITGLLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EGTRDLVEFNEKWQQNQTARATTQSRVSLKEAIAASVSRGKLVSGSSGANPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 124;
  LYAIYLIVIGLSGG--FMVLYYVSLRF
                                                                                                                                                                                                                                                                                                                                                                               -GFLYFGHGSIOLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLY
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26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ATP-binding cassette protein F12L6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 2.4e-38;
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                                                                                                                                                                                                                                                                                                                                  -----FYCCADNIPVFIQERYIFL
664
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                                                                                      GDKILSAMELDSY
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103 107

664

PDLLMQQGITQLSKWDCLWITLAWGLFFRILFYLSLLF 701

599

603

539

483

638

442

431 388 381 336

479

RyFavello, A.; Scheet, P.
submitted to the EMBL Data Library,
submitted for the sequence of C. el A; Description: The sequence A; Reference number: Z21104 A; Accession: T31958 hypothetical protein F02E11.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te C; Accession: A; Status: preliminary; type: DNA T31958 translated elegans from GB/EMBL/DDBJ July 29-Oct-1999 #text_change cosmid F02E11 31-Jan-2000

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A:Introns: 115/3; 158/3; 214/3; 330/3; 368/2; 448/3; 525/1
C:Superfamily: fruit fly white protein; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ş
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A;Cross-references: EMBL:AF016661; PIDN:AAB66050.1; GSPDB:GN00020; CESP:F02E11.1
A;Experimental source: strain Bristol N2; clone F02E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26...
180; Conservative 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
Gene: CESP:F02E11.1
                                                   640 LYAIYLI-----VIGLSGGFMVLYYVSLRFIK 666
                                                                                                                                                                                                                  519 WVAVSIAYVGACIFGDEGLVVTF-MPMFVLPML----VFGGFYVNANS---IPVYYQYV 569
                                                                                                                                                                                                                                                                                          536
           628
                                                                                                                      570
                                                                                                                                                        594 SFLRWC---FEGLMKIQFSRRTYKM------PLGNLTI----AVSGDKILSAMELDSYP 639
                                                                                                                                                                                                                                                                                                                            459 REHKSNIYSVEAYFLAKSLAELPQYTILPMIYGTIIYWMAGLVASVTSFLVFVFVCITLT 518
                                                                                                                                                                                                                                                                                                                                                                             480 YELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQFFLLH----FLLV 535
                                                                                                                                                                                                                                                                                                                                                                                                                                          402 QILATAILVGIV---NWRVELKGPTIQNLEGVMYNCARDMTELFYFPSVNVITSELPVFL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 EACLMSMTIGFLYFGHGSIQL---SFMDTAALLFMIGALIPFNVILDVISKCYSERAMLY 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 GDDEDDGESRYNSTFGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 AETKOLDEDTCVESSVTPLDTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPTLLIHGA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 VPESYNPADFVMSETSISPET-EQEDVTRIEYLIHEYQNSDIGTQMLKKTRTAVDEFGGY 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 CPRYSNPADFYVDLTSIDRRSREQELATR-----EKAQSLAALFLEKVRD-LDDFLWK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 RALLDLANKGKTIIVVLHQPSSTVFRMFHKVCFMATGKTVYHGAVDRLCPFFDKLGPDFR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 KTLSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIG--YP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 DMNLTDCQNTLIGIPNRMKGISIGEKKRLAFACEILTDPKILFCDEPTSGLDAFMASEVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 ELRLRQCADTRVG-NMYVRGLSGGERRRVSIGVOLLWNPGILILDEPTSGLDSFTAHNLV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 VNGKKITKOKMROMCAYVOOVDLECGTLTVREQLTYTAHMRNKNATVQ-QKMERVENVLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 INGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 PSCQNSCELGIQNLSFKV----RSGQMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQIW 133
                                                                                                       SFVSWFKHGFEALEANOW-KEIDKISGCDLINPLNATTTGYCPASDGPGILTRRGIDT-P 627
                                                                                                                                                                                                                                                       WILVVECCRIMA--LAAAALLPTEHMASEFSNALYNSEYLAGGEMINLSSLWTVPAWISKV 593
LYANVLILEMSEFVYRIIGL-----VALKIRVRFAK 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PECLAVCALPTSSYQISVSGVAEPGEVLALMGGSGAGKTTLMNILAHLDTNGVEYLGDVT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.5%; Score 579; DB 2; 28.3%; Pred. No. 8.5e-38; vative 113; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----QFEILLKRSLRTTFRDPLLLRVRFA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86;
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Search completed: July 25, 2003, 17:15:32 Job time: 46 secs

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                       2871
2835.5
742
739.5
735.5
735.5
730.5
723.5
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700
695.5
668.5
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length: 2000000000
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Match
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11:
12:
13:
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    830525 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAGKAAEERGLPKGATPQDT.....FMVLYYVSLRFIKQKPSQDW 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-989-981A-8
3506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                  sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                                                                             sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_mammal:*
sp_mhc:*
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sp_bacteria:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_tungi:*
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sp_archeap:*
                                                                                                                                                                                                                                                                                                                                          sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                           sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                    sp_plant:*
                                                                                                                                                                                                           Length DB
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                                                                                                                                     10
    Q9NH94
Q93YS4
                                                   Q8T691
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                                                                                                            Q8R543
Q8CIQ5
Q9ARU4
Q9L182
Q9ZU35
Q9ZU35
Q9ASR9
Q9C6W5
                           Q9FT51
Q9R004
                                                                          Q8CIQ4
Q949Y4
                                                                                                  Q9C6R7
                                                               Q9C8W6
                                                                                                                                                                                                                                             SUMMARIES
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                                               Q949y4 arabidopsis
Q9c8w6 arabidopsis
Q8t691 dictyosteli
                                                                                                                                Q8ciq5 rattus norv
Q9aru4 oryza sativ
Q9li82 arabidopsis
Q9zu35 arabidopsis
                                                                                           Q9asr9 arabidopsis
Q9c6w5 arabidopsis
Q9c6r7 arabidopsis
                                                                                                                                                                                                      Description
                       Q9ft51 arabidopsis
Q9r004 mus musculu
Q93ys4 arabidopsis
                                                                                  Q8ciq4 rattus norv
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O8R543;
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
O1-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                             Sterolin 2. ABCG8.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=129/Sv:
                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

NCBI_TaxID-10090;
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45	44	43	42	41	40	39	38	37	36	35	4	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
579.5	~	582	582	586.5	589.5	590.5	591	595	595	597.5	598.5	607.5	610.5	612.5	613	616.5	617.5	621	621.5	634.5	642.5	642.5	642.5	643	647.5	651.5	.653	658
•	16.5	16.6	16.6		16.8	16.8	16.9	17.0	17.0	17.0	17.1	17.3	17.4	17.5	17.5	17.6	17.6	17.7	17.7	18.1	18.3	18.3	18.3	18.3			18.6	
646	627	1509	1328	708	720	610	725	723	687	692	785	703	609	669	594	691	669	666	567	655	679	655	655	670	679	635	656	687
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Q8K4E1	Q91WA9	Q8T688	Q9NGP5	Q9M2V5	Q9M2V7	P90746	Q9M3D6	Q8LNT5	Q9C8K2	P91892	Q96L76	QBRXN0	Q9VQN4	Q8WRR1	Q9LJC3	Q8RWI9	Q8WRF2	Q9EPG9	Q9FG17	Q96LD6	Q9вн97	Q8IX16	Q96TA8	077423	Q8IS30	Q9SZR9	Q8MIB3	Q94960
Sum	mus.	Q8t688 dictyosteli	a.		7	a			N		Q96176 homo sapien	0		~			Q8wrf2 tribolium c		7				_			9		. Q94960 drosophila
musculu	musculu	steli	steli	arabidopsis	arabidopsis	habdi.	arabidopsis	oryza sativ	arabidopsis	aegyp	apien	dopsis	hila	Lium c	arabidopsis	arabidopsis	i III	rattus norv	arabidopsis		itis c	homo sapien	homo sapien	cera	cera	arabidopsis	rofa	ohila

ALIGNMENTS

Created)
Last sequence update)
Last annotation update)

PRT;

673 AA

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Query Match 81.9%; Score 2871; DB 11; Length 673;	SQ SEQUENCE 673 AA; 76008 MW; FA08340445DF259C CRC64;	DR PROSITE; PS00211; ABC_TRANSPORTER; 1.	DR ProDom; PD000006; ABC_transporter; 1.	DR Pfam; PF00005; ABC_tran; 1.	DR InterPro; IPR003439; ABC_transporter.	DR EMBL; AF351810; AAL82898.1; JOINED.	EMBL; AF351809; AAL82898.1;	••	EMBL; AF351807; AAL82898.1;	EMBL; AF351805; AAL82898.1;	EMBL; AF351804; AAL82898.1;	EMBL; AF351803; AAL82898.1;	EMBL; AF351802; AAL82898.1;	EMBL; AF351801; AAL82898.1;	EMBL; AF351800; AAL82898.1;	EMBL;	DR EMBL; AF351811; AAL82898.1;	RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.	RT mouse head-to-head tandem ABC transporters.";		RA Lu K., Zhou Y., Lee MH., Patel S.B.;	RC STRAIN=129/Sv;
Length 673;	CRC64;								,			-		•				tabases.		terization of novel		

DB 11; Length Indels

672; <u>سر</u> ۰۰

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Matches
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Q8CIQ5;
Q1-MAR-2003
Q1-MAR-2003
Q1-MAR-2003
Sterolin 2.
   STRAIN-Sprague-Dawley;
Yu H., Lu K., Lee M., Pandit B., Patel S.B.;
"The rat Abcg5 and Abcg8: characterization,
genetic variation in sitosterolemic rats,";
Submitted (AUG-2002) to the EMBL/GenBank/DDB.
EMBL; AY145899; AAN64276.1;
                                                                                                                                         Rattus norvegicus (Rat).
Rattus norvegicus (Chordata;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                           ABCG8
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51; Conservative 5
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HGSEACLMSLIIGFLYYGHGAKQLSFMDTAALLFMIGALIPFNVILDVVSKCHSERSMLY
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                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                         Murinae;
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Best Local's
Matches 538
                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; S
Spermatophyta; Magnoliophyt
Ehrhartoideae; Oryzeae; Ory
NCBI_TaxID=4530;
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O9ARU4;
O1-JUN-2001 (
O1-JUN-2001 (
O1-MAR-2003 (
Putative ABC
P0445D12.3.
SEQUENCE FROM N.A. STRAIN-cv. Nipponb Sasaki T., Matsumc
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538; Conserv
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 Matsumoto
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1 (TrEMBLrel. 17,
3 (TrEMBLrel. 23,
               Nipponbare;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       672 AA;
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                  transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                          Magnoliophyta;
Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75906 MW;
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 Yamamoto
                                                                                                   Streptophyta;
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                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                Created)
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Pred. No. 2.1e-
                                                                                      Liliopsida;
                                                                                                                                                                                                                              PRT;
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7.
                                                                                                     Embryophyta; Tracheophyta;
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                                                                                         Poales;
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480

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599 600 420

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300 300 240 180 120

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DT 01
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Best Local Similarity
Matches 188; Conserv
            Q9LI82 PRELIMINARY; PKT; 0/2 AA.
Q9LI82;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABC transporter-like protein.
ABC transporter-like protein.
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InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1. clone:P0445D12.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
EMBL; AP003046; BAB40032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gramene; Q9ARU4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIGYPCPRYSNPADFYVDLTSIDRRSREQELATREKAQSLAALFLEKVRDLDDFLWKAET 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAEKVMETLRQLAEDGHTVICSIHQPRGSVYGKFDDIVLLSEGEVIYMGPAKEEPLLYFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRILMFWYWLTYLLLKKNRP
                                                                                                                                                                                                                                                                                                                                                             CFEGLMKIQF-----SRRTYKMPLGNLTIAVSGDKILSAMELDSYPLYAIYLIVIGLSG
                                                                                                                                                                                                                                                                                                                                                                                                      SPAASAMGLTVGAMAPTTEAAMALGPSLMTVFIVFGGYYVNPDNTPVIFRWIPKVSLIRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRERAKGSYALGPYLSSKLLAEIPIGAAFPLIFGSILYPMSKLHPTFSRFAKFCGIVTVE
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                                                                                                                                                                                                                                                                                    GFMVLYYVSLRFI - - - KQKP
                                                                                                                                                                                                                                                                                                                       AFQGLCINEFKGLQFEQQHSYDIQTGE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WARITCALKNKRGDVARFLLSNASGEAKSGRLLALMGPSGSGKTTLLNVLAGQLTASPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WTSPSCQNSCELG-----IQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGR--GHGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 124; Mismatches 252;
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Pred. No. 1.8e-49;
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                                                   update)
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Best Local Sim
Matches 221;
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Sequence features of the regions of 4,251,695
TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 7:217-221(2000).
EMBL; AP001313; BAB03081.1; -
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR006162; Ppantne_attach.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding.
SEQUENCE 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embry, Spermatophyta; Magnoliophyta; eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabi, NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20363099; PubMed=10907853;
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Kaneko T., Kato T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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TVGDLPMELILPTIFVTITYWMGGLKPSLTTFIMTLMIVLYNVLVAQGVGLALGAILMDA
                                                                                                                                                                                                                                                                                                                               YRMFDKVLVLSEGCPIYSGDSGRVMEYFGSIGYQPGSSFVNPADFVLDLANGITSDTKQY
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                                                                                                                     GHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELEDGLYTTGPYFFAK
                                                                                                                                                                       AITNRWPTSWWM----
                                                                                                                                                                                                       --TNCLPSPTKMPGAVQQFTTLIRRQIS----NDFRDLPTLLIHGAEACLMSMTIGFLYF
                                                                                                                                                                                                                                              DQ-IETNGRLDR-----LEEQNSVKQSLISSYKKNLYPPLKEEVSRTFPQDQTNARLRKK
                                                                                                                                                                                                                                                                                         EQELATREKAQSLAALFLEKVRDLDDFLWKAETKDLDEDTCVESSVT-PLD------
                                                                                                                                                                                                                                                                                                                                                                      FRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGY-PCPRYSNPADFYVDLT---SIDRRSR
                                                                                                                                                                                                                                                                                                                                                                                                                 ERKRVSIGQEMLVNPSLLLLDEPTSGLDSTTAARIVATLRSLARGGRTVVTTIHQPSSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                        ERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRLVLISLHQPRSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYPHLTVMETLTYTALLRLPKELTRKEKLEQVEMVVSDLGLTRCCNSVIGGGLIRGISGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILKFEELTYSIKSQTGKGSYWFGSQEPKPNRLVL-----KCVSGI-----VK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLEVRDLNYQVD------LASQVPWFEQLAQFKMPWTSPSCQNSCELGIQNLSFKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QESSFPKTPSANRHETSPVQENRFSSPSHVNPCLDDDNDHDGPSHQSRQSSVLRQSLRPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EERGLPK--GATPQDTSGLQDRLFSSES------DN------SLYFTYSGQPN 45
                                                                                 -HSRV-AHLQDQVGLLFFFSIFWGFFPLFNAIFTFPQERPMLIKERSSGIYRLSSYYIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    %; Score 739.5; DB 1
%; Pred. No. 2.8e-49;
126; Mismatches 251
                                                                                                                                                                -QFSVLLKRGLKERSHESFSGLRIFMVMS-----VSLLSGLLWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Nakamura Y., Asamizu E., T
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20B2D99215600135 CRC64;
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bp covered
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE-20083487; PubMed-10617197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Pfam; PF00005; ABC_tran; 1
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E; PS00211; ABC_TRANSPORTER;
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01-JUN-2001 (Tremblr
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At2g01320/F10A8.20.
                     Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B
Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
Palm C.J., Pham P.R., Quach H.L., Sakano H., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis CDNA clones";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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3 (TremBLrel. 23,
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ABC_transporter.
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Best Local Similarity
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                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (ABC transporter, putative)...
E27M3_2 OR ATIG311710/E27M3_2.
                                                                                                                                                                                                                             Q9C6W5;
       SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed-11130712;
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ProDom; PD000006; ABC_transporter;
PROSITE; PS00211; ABC_TRANSPORTER;
ATP-binding; Transport.
SEQUENCE 725 AA; 78998 MW; 68A;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci Hayashizaki Y., Shinozaki K., "Arabidopsis thaliana full-length cDNA."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases EMBL; AC074350; AAG60152.1; EMBL; AV088793; AAM67104.1; EMBL; AX117530; BAC42192.1; InterPro; IPR003439; ABC_transporter.
                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 648 AA; 72618 MW;
                                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD000006; ABC_transporter; 1. PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00005; ABC_tran;
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Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis thallana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV.
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White O., Alonso J., Altafi H.,
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TAHRIVTTIKRLASGGRTVVTTIHQPSSRIYHMFDKVVLLSEGSPIYYGAASSAVEYFSS
                   TAHNLYKTLSRLAKGNRLYLISLHQPRSDIFRLFDLYLLMTSGTPIYLGAAQHMYQYFTA
                                                            HVDRVIAELGLNRCTNSMIGGPLFRGISGGEKKRVSIGQEMLINPSLLLLDEPTSGLDST
                                                                          TFSGKVMYNGQPFSGCIKRR-TGFVAQDDVLYPHLTVWETLFFTALLRLPSSLTRDEKAE
                                                                                                                                      IKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDK
                                                                                                                                                                                 QGLPDMSDTQSKSVLAFPTITSQPGLQMSMY-----PITLKFEEVVYKVKI-----E
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a A., Narusaka
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ka M., Carninci
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                                                                                                                                                                                                                                                                                                         269;
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MEDINE-21016719; pubMed-11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Fong B., Fujii C.Y.,

Bunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
                                          InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; AAA_ATPase.
Pfam; PF00005; ABC_transporter.
Proc. PF00005; ABC_tran: 1
                                                                                                                                                                                                                             Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriuni M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.W.D., Yu G., Fraser C.M., Venter J.C., Davis R.W., Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2001 (TREMBLIEL 17
01-MAR-2003 (TREMBLIEL 23
ABC transporter, putative.
   SMART; SM00382;
                                                                                                                                                  Nature 408:816-820(2000).
EMBL; AC079041; AAG50724.
                                                                                                                                                                                                             Wu D., Yu G., Fraser C. "Sequence and analysis thaliana.";
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RESULT 9 Q8CIQ4

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ABCG5 Sterolin

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Sciurognathi; Muridae;

Muridae;

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Euteleostomi;

Rattus norvegicus (Rat).

NCBI_TaxID=10116;

STRAIN=Sprague-Dawley; SEQUENCE FROM N.A. 01-MAR-2003 01-MAR-2003 01-MAR-2003

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Matches 208
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                                                                                                                              MALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVP---AWISKVSFLRWCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WKSKE----KTILNGITGMVCPGEFLAMLGPSGSGKTTLLSALGGR--LSKTFSGKVMY
                                                                                  GLMKIQFSRRTY---
                                                                                                                                                                       GMYRLSSYFMARNVGDLPLELALPTAFVFIIYMMGGLKPDPTTFILSLLVVLYSVLVAQG
                                                                                                                                                                                                                                                                                                                                                              SNPADFYYDLTS----IDRRSREQELATREKAQSLAALFLEKYRDLDDFLWKAETKDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRLRQCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKT
                           YLIVIGLSGGFMVLYYVSLR
                                                      LLLGIQYTDDDYYECSKGVWCRVGDFPAIKSMGLNNLWI----
                                                                                                             LGLAFGALLMNIKQATTLASVTTLVFLIAGGYYVQ-----QIPPFIVWLKYLSYSYYCYK
                                                                                                                                                                                                  GLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRI
                                                                                                                                                                                                                             VISVAFLGGLLWWH-TPKSHIQDRTALLFFFSVFWGFYPLYNAVFTFPQEKRMLIKERSS
                                                                                                                                                                                                                                                         CLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELED
                                                                                                                                                                                                                                                                                                                 EDTCVESS----VTPLDTNCLPSPTKMPGAVQQFTTLIRRQI-SNDFRDLPTLLIHGAEA
                                                                                                                                                                                                                                                                                                                                                                                                                     LSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTESQAQRDKRVEDVIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLPD-MSDTQSKSVLAFPTITSQPGLQMSMYPITLKEVVYKVKI-----EQTSQCMGS
                                                                                                                                                                                                                                                                                       AELCNAESHSYEYTKAAAKNLKSEQWCTTWWYQFTVLLQRGVRERRFESFNKLRIF---Q
                                                                                                                                                                                                                                                                                                                                               VNPADLLLDLANGIPPDTQKETSEQEQKTVK--ETLVSAYEKNI-----STK-LK 350
                                                                                                                                                                                                                                                                                                                                                                                                       IKRLASGGRTVVTTIHQPSSRIYHMFDKVVLLSEGSPIYYGAASSAVEYFSSLGFSTSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLNRCTNSMIGGPLFRGISGGEKKRVSIGQEMLINPSLLLLDEPTSGLDSTTAHRIVTT
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-YMALHRVKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.6%; Score 723.5; 30.6%; Pred. No. 4.
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646
                            663
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ches 262;
                                                                                  -KMPLGNLTIAVSGDKILSAMELDSYPLYAI 643
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                                                      -DVFVMGVMLVGYRLMA-
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                                                      636
                                                                                                                                           601
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RESULT OPERIOR RESULT OPERIOR PROPERTY OF THE 
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Best Local S
Matches 190
                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                       Q949Y4;
Q949Y4;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative ABC transporter protein.
        SEQUENCE FROM N.A.
Yamada K., Liu S.X.,
                                                                                                                                                                                                                                                                                                       Q949Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRAVSDQESQDGLYQKWQMLLAYVLHALPFSIVATVIFSSVCYWTLGLYPEVARF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERAMLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVIMRLVQNLIMGLFLIFYLLRVQNNMLKGAVQDRVGLLYQLVGATPYTGMLNAVNLFPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIRNIEEMPIPLKILGYFTFQKYCCEILVVNEF
                                                                                                                                                                                                                                                                                                                                                                                                                         FMINLSSLWTVPAWISKVSFLRWCFEGLMKIQF 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVWLVVFCCRIMALAAALLPTFHMASFFSNAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLLIHGAEACLMSWTIGF--LYFGHGSIQLSFMDTAALLFWIGALIPFNVILDVISKCYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDFLWKAETKDLDEDTCVESSVTPLDTNCLPSPTK-MPGAVQQFTTLIRRQISNDFRDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPCPRYSNPADFYVDLTSIDRRSREQELATREKAQSLAALF------LEKVRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIVLLLYELARRNRIVIVTIHQPRSELPHHFDKIAILTYGELVFCGTPEEMLGFFNNCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNLVKTLSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDVIAELRLRQCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPCPEHSNPFDFYMDLTSVDTQSREREIETYKRVQMLESAFRQSDICHKILENIERTRHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAVLTELSLSHVADQMIGNYNFGGISSGERRRVSIAAQLLQDPKVMMLDEPTTGLDCMTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEGARGPHNURGSQ----SSLEEGSV--TGSEARHSLGV--LNVSFSVSNRVGPW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKGAT-PQDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLASQV-PWFEQLA
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.3%; Score 713; DB 11;
Llarity 30.0%; Pred. No. 3.2e-47;
Conservative 115; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GYFSAALLAPHLIGEFLTLVLLGMVQNPNIVNSIVALLSISGLLIGSG
          Pham
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        P.K.,
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        Banh
      J.,
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      Banno
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    Dale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YNSFYLAGG
                                                                                                         Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RA Tang C., Toriumi M., Yamamura Y., Yu.G., Yu.S., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A;
RT "Full Length cDNA of gene F17M19.11 (GI:12324545).";
RI Submitted (AUG-2001) to the EMEL/GenBank/DDBJ databases.
DR EMBL; AV605010; AAK92745.1; -
DR InterPro; IPR003439; ABC_transporter.
DR Ffam: PF00005; ABC_transporter.
DR Pfam: PD00006; ABC_transporter: 1.
DR SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sir
Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00382; AAA;
ATP-binding.
SEQUENCE 662 AA;
                   11
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                                                                                                                                                          CYRLLVAIQYG
                                                                                                                                                                                              CFEGLMKIQFSRRTYKMPLGNLTIAVSGDKILSAMELDSYPLYA---
                                                                                                                                                                                                                                                                            CRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPA---WISKVSFLRW
                                                                                                                                                                                                                                                                                                                    RASGMYTLSSYFMAHVLGSLSMELVLPASFLTFTYWMVYLRPGIVPFLLTLSVLLLYVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                          LMSMTIGFLYFGHGSIQLSFMDTAALLFMI----GALIPFNVILDVISKCYSERAMLYYE
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                                                                           IGDVGMWTSVGVLFLMFFGYRVLAYLALRRIK
                                                                                                                     IGLSG-----
                                                                                                                                                                                                                                     SQGLGLALGAAIMDAKKASTIVTVTMLAFVLTGGYYVN-----KVPSGMVWMKYVSTTFY
                                                                                                                                                                                                                                                                                                                                            LEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFC
                                                                                                                                                                                                                                                                                                                                                                                                      AASILCGLMWW-HSDYR-DVHDRLGLLFFISIFWGVLPSFNAVFTF----PQERAIFTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIDRRSREQELATREK----AQSLAALFLEKVRDLDDFLWKAETKDLDEDTCVESSVTPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTSIHQPSSRVFQMFDTVLLLSEGKCLFVGKGRDAMAYFESVGFSPAFPMNPADFLLDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NARFVKTRYNGG--GITTCIATWFSQLCILLHRLLKERRHESFD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             662 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72903 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107;
                                                                                                               -GEMVLYYVSLRFIK 666
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----IXLIV

647 584 598 529 ----LLRIFQVV

325

265

206 141

382 365

469 481 415 425 233;

136;

Gaps

82

Length 662; Indels

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With E-21016719; Pubmed-11130712;

With E-21016719; Pubmed-11130712;

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buchler E., Chan A., Chao Q., Chen H., Cheuk R.E., Chin C.W.,

White O., Alonso J., Altafi H., Cheuk R.E., Chin C.W.,

White O., Alonso J., Altafi H., Cheuk R.E., Chin C.W.,

White O., Chan A., Chao Q., Chen H., Cheuk R.E., Chin C.W.,

White O., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

White O., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

White O., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

White O., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

White O., Militan S., Johnson-Hopson C., Khan S., Khaykin E.,

White O., Feldblyum T.V., Feng J.-D., Khan S., Khaykin E.,

White O., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

White O., Feldblyum T.V., Feng J.-D., Wanti R., Warnan H.,

White O., Feldblyum T.V., Feng J.-D., Maiti R., Wan A., Lam B.,

Langin H., Shin E., Liu J., Liu Y.-P.,

White O., Feldblyum T.V., Feng J.-D., Walker M.,

White O., Feng J., Walker M., Walker M.,

White O., Feng J., Walker M.,

White O., Walker M.,

Walker M.,

White O., Walker M.,

Walker 
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Best Local Similarity

Matches 210; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:816-820(2000).
EMBL; AC021665; AAG52231.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative ABC transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
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               404
                                                                                      293
                                                                                                                                                              355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 FSQAQRDKRVEDVIAELRLRQCADTRVGNMYVRGLSGGERRRVSIGVQLLMNPGILILDE 238
                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                    298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 TGRGHGGKIKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SNDSCNIKKLLGLKQKPSDETRSTEERTILSGVTGMISPGEFMAVLGPSGSGKSTLLNAV
                                                                                                                              LTRDVKLRAAESVISELGLTKCENTVVGNTFIRGISGGERKRVSIAHELLINPSLLVLDE 179
-----RRQISNDFRDLPTLLIHGAEACLMSMTIGFLYFGHGSIQLSFMDTAALLFMI--
                                                                           ---DTLLAPQVK-----TCIEVSHFPQD-NARFVKTRVNGG--GITTCIATWFSQLCILL 341
                                                                                                                                                                                                                     RDAMAYFESVGFSPAFPMNPADFLLDLA--NGVCQTDGVTEREKPNVRQTLVTAY-----
                                                                                                                                                                                                                                                                                            QHMVQYFTAIGYPCPRYSNPADFYVDLTSIDRRSREQELATREK---AQSLAALFLEKVR 354
                                                                                                                                                                                                                                                                                                                                                                       PTSGLDATAALRLVQTLAGLAHGKGKTVVTSIHQPSSRVFQMFDTVLLLSEGKCLFVGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                              PTSGLDSFTAHNLVKTLSRLAKG*NRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGRIHGSNI-TGKILINDGKITKQTLKR-TGFVAQDDLLYPHLTVRETLVFVALLRIPRS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 AA; 67007 MW; 65DllA874E5C0B61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABC_tran; 1
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31.8%; Pred. No. 3.1e-46;
tive 103; Mismatches 225; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huizar L.,
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VDNIKNNE 435	376 INTQVEDQADSDDDDYNDEEEEIGGGGGGGGGGGGGIEDIGISISPTMNGSAVDNIKNNE	₽
ID 328	325TSID	Qy
PADFYVDL 324 :: PADFFLDL 375	265 YLISHIJPKBITKLFÜLYLLMTSGTPIYLGAAQHMYQYFTAIGYPCPRYSNPADFYYDL :: :: : : : : :: :	B &
	56	DЬ
RLAKGNRL 264	207NMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRL	Qy
RCADTLVG 255	196 LCGYVTQSDSLMPSLTVRETLNFYAQLKMPRDVPLKEKLQRVQDIIDEMGLNRCADTLVG	В
	147 CVAHVROHNOLLPNLTVRETLAFIAOMRLPRTESOAORDKRVEDVIAELRLR	Qy
SDFNIFKK 195	139 LTNINGHIESGTIFAIMGPSGAGKTTLLDILAHRLNINGSGTMYLNGNKSDFNIFKK	DЪ
SSPQLVRK 146	င္အ	Qy
; Gaps 20;	Query Match 19.8%; Score 695.5; DB 5; Length 801; Best Local Similarity 27.9%; Pred. No. 1e-45; Matches 187; Conservative 134; Mismatches 230; Indels 119;	* H.O.
	ATP-Dinding; Transport. SEQUENCE 801 AA; 90052 MW; CCC4F0036CB195A3 CRC64;	SQ
	PROSITE; PS00211; ABC_TRANSPORTER; 1.	DR
	Probable (2003) ABC_transporter; 1.	DR S
	Pro: IPRO03439; ABC	
	100003503; han ambase	尿尿
	(FEB-2002) to the EMBL/GenBa RITY: BELONGS TO THE ABC TRA	CC
	"Evolution of the ABC transporters of Dictyostelium.";	RA
	Ax4;	R
•	[1] SEQUENCE FROM N.A.	R.R.
		28
	m (Slime mold	လ လ
	ansporter AbcG1.	B
	2002 (Tremburel. 21, Last sequence up	33
	002 (Tremaire) 21	DA PA
	08T691 PRELIMINARY; PRT; 801 AA.	I S
	SULT 12	RE
YLALRRIK 608	549 RMLGCDSKGKQGASAATSAGCREVEEEVIGDVGMWTSVGVLFLMFFGYRVLAYLA	DЪ
GEMVLYYVSLRFIK 666	631 SAMELDSYPLYAIYLIVIGLSGGEMVLY	γQ
:: SGEEIL 548		DЬ
AVSGDKIL 630	574 GGFMINLSSLWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVSGDKII	Ω¥
	449 FTYWMYYLRPGIVPFLLTLSVLLLXYLASQGLGLALGAAIMDAKKASTIVTVTMLAFVLT	밁
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                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 189
                                                                                                                                                                                                                                                                                                                         ATP-binding.
737 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; agnoliophyta; endicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicales; Rosan washidante.
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01-MAR-2001 (TIEMBLIEL 16, Last sequence update)
01-MAR-2003 (TIEMBLIEL 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000006; SMART; SM00382; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL132972; CAC07922.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003593; AAA_ATPASe.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eurosids II; Brassicales; Brassicaceae; NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                               Similarity
     DILEDIEAATSSVVKFQAEPTFPIYLKFIDITYKV--
                                                                                                                                                              DRLFSSESDNSLYFTYSGQPN----TLEVRDLNYQVDLASQVPWFEQLAQFKMPWTSPSCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSL--WTVPAWISKVSFLRWCFE 601
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                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                          81770 MW;
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                                                                                                                                                                                                                                                    19.1%; Score 668.5; DB 1
28.0%; Pred. No. 1.2e-43;
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                                                                                                                                                                                                                                                                                                                                    A22689E5EBEBCB50 CRC64;
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                                               EMBL; AF140218; AAD54216.1; -...
MGD; MGI:1347061; Abcg2.
InterPro; IPR003593; AAA_ATPASe.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR006162; Ppantne_attach.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9R004 PRELIMINARY; PRT;
Q9R004;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequ
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation of the content of t
                                                                                                                                                                                                                                                                                     STRAIN-FVB; TISSUE-Liver;
MEDLINE-99413474; pubMed-10485464;
Allen J.D., Brinkhuls. R.F., Wijnholds J., Schinkel A.H.;
"The mouse Bcrpl/Mxr/Abcp gene: amplification and overexpression : cell lines selected for resistance to topotecan, mitoxantrone, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABCG2 OR BCKr..
ABCG2 OR BCKr..
Mus musculus (Mouse).
Metazoa; Chordata;
Aberia; Rodentia;
        PROSITE;
                                 ProDom; PD000006;
SMART; SM00382; A
                                                                                                                                                                                                                                         doxorubicin.";
Cancer Res. 59:4237-4241(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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PS00012; PHOSPHOPANTETHEINE;
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Best Local Similarity
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                 Q9NH94
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SEQUENCE 657
                         SEQUENCE FROM N.A.
STRAIN-Kin-Shiu X Sho-wa;
MEDLINE-20469043; PubMed-11016828;
MEDLINE-20469043 Fubmed-1 T. Kanda T.
                                                                                                                    Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bon
Bomburdas.
                                                                                                                                                                             ATP dependent transmembrane
Tamura T.;
"Identification and characterization of a silkworm ABC transporter
                                                                                                           Bombycidae; Bombyx.
                                                                                               NCBI_TaxID=7091;
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transporter protein.
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MO1. Gen. Genet. 264:1-19(2000).
-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
EMBL; AF229609; AAF61569.1; -
InterPro; IPR003593; AAA_ATPase.
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SEQUENCE 687 AA; 75835 MW; ECD336333F0981AB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PGRLKGISGGEMKRLSFASEVLTDPPLMFCDEPTSGLDSFMAQNVIQVLKGLAQKGKTVV
AGVETIACTRENFTCPASGQVVLETLSFSQDDFAMDVVNMILLFV--GFRFLAYLAL
                              SR-RTYKMPLGNLTIAVSGDKILSAMEL--DSYPLYAIYLIVIGLSGGFMVLYYVSL 662
                                                                                          LLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCF---EGLMKIQF 608
                                                                                                                                                        YFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALAAAA 551
                                                                                                                                                                                                                       GFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELEDGLYTTGP 491
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                                                            ASSSVSMAASVGPPIIIPFMLFGGFFLNSGS---VPPYLSWISYLSWFHYGNEALLINOW
                                                                                                                          YFLSKTLAEAPVFATIPLVFTTIAYYMIGLNPDPKRFFIASGLAALVTNVATSFGYLISC
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IPR005284; Pigment_permease.
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Search completed: July 25, Job time: 115 secs 2003, 17:14:44

Copyright

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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        1.1 US-09-989-981A-8
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US-09-837-992-3
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1.1 US-09-87-992-1
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1.1 US-09-86-866A-14
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Sequence 8, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 245, Appl
Sequence 35, Appl
Sequence 16, Appli
Sequence 17, Appli
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US/09-989-981A-8
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09989981A Publication No. US20030049730A1 GENERAL INFORMATION:
                                                                                                                                                                   Matches
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tularik Inc.
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION UMBER: US 60/252,235
PRIOR PRIOR DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hobbs, Helen H. APPLICANT: Shan, Bei APPLICANT: Barnes, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: human ABCG8 (hABCG8)
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Tian, Hui
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115 US-10-003-357-1335
115 US-10-009-455-4
115 US-10-154-452-8
115 US-10-154-452-8
114 US-10-154-452-9
115 US-10-090-455-2
115 US-10-090-455-2
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115 US-10-050-453A-2
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115 US-10-050-453B-5
115 US-10-050-338B-5
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0; Mismatches
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Minimum DB Maximum DB

Scoring table: Sequence: Title: Perfect score:

Database

Result

Score

Match Query

Length

10: 111: 12: 12: 13: 14: 14: 15: 16: 16: 17:

3502 2883.5 697

688.5 688.5 666 656 642.5 642.5 642.5 638.5

61 QVPWFEQLAQFKMPWTSPSCQNSCELGIQNLSFKVRSGQMLAIIGSSGCGRASLLDVITG

100.0 99.9 182.2 19.9 19.9 19.6 19.6 19.6 19.6 19.6 19.0 18.7 18.3

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Best Local S
Matches 672
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Publication No. US20030027259A1
GENERAL INFORMATION:
APPLICANT: Chen, Hongyun
APPLICANT: Le Bihan, Stephane
TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND USES THEREOF
FILE REFERENCE: 100103.406
CURRENT APPLICATION NUMBER: US/10/090,455
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 7 LENGTH: 673
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QVPWFEQLAQFKMPWTSPSCQNSCELGIQNLSFKVRSGQMLAIIGSSGCGRASLLDVITG
                                                    MAGKAAEERGLPKGATPQDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLAS 60
                                       MAGKAAEERGLPKGATPQDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLAS
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Pred. No. 0;
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US-09-989-981A-4
                                       NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2
SEQ ID NO 4
LENGTH: 672
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER IMFORMATION: mouse
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                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
 Query Match
                                                                                                                                                                                                             APPLICANT: Tian, Hui
APPLICANT: Tularik Inc.
APPLICANT: Board of Regents, The Universit
TITLE OF INVENTION: ABCG5 and ABCG8: Compo
EILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/253,645
                                                                                                                                                         PRIOR FILING DATE: 2000-11-28
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APPLICANT: Shan, Bei
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                                           ABCG8
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 Score 2883.5;
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Length 672;

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TITLE OF INVENTION: SITOSTEPOLEMIA SUSCEPTIBILITY Gene (SS TITLE OF INVENTION: and Methods of Use FILE REFERENCE: 018781-006020US CURRENT APPLICATION NUMBER: US/09/837,992 CURRENT FILING DATE: 2001-04-18 PRIOR APPLICATION NUMBER: US 60/198,465 PRIOR FILING DATE: 2000-04-18 PRIOR FILING DATE: 2000-04-18 PRIOR FILING DATE: 2000-05-15 NUMBER OF SEQ ID NOS: 45 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tian, Hui
APPLICANT: Schultz, Joshu
APPLICANT: Shan, Bei
APPLICANT: Tularik Inc.
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Patent No. US20020081687A1
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US-09-837-992-3
                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                    Sequence 6, Application US/09989981A Publication No. US20030049730A1
        APPLICANT: Hobbs, Helen H.
APPLICANT: Shan, Bei
APPLICANT: Barnes, Robert
APPLICANT: Tian, Hui
APPLICANT: Tian, Hui
APPLICANT: Tularik Inc.
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Method
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CCURRENT FILING DATE: 2002-07-23
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/252,235
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124; Mismatches 241
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; OTHER INFORMATION: human ABCG5 (hABCG5)
US-09-989-981A-6
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PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                    Sequence 6, Application US/10090455 Publication No. US20030027259A1 GENERAL INFORMATION:
APPLICANT: Chen, Hongyun
APPLICANT: Chen, Stephane
APPLICANT: Le Bihan, Stephane
TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND USES
FILE REFERENCE: 100103.406
CURRENT APPLICATION UNDER: US/10/090,455
CURRENT APPLICATION UDDER: US/10/090,455
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                                                                                                                                                                                                                                                                                                                                           -GYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFL
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US-09-837-992-1
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SOFTWARE: FastSEQ for
SEQ ID NO 6
LENGTH: 651
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Best Local :
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                                                                       RNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTN
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                                                                                                                                                                                 WLVVFCCRIMALAAALLPTFHMASFFS----
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for Windows Version
                                                                                                                                          -GYFSAALLAPHLIGEFLTLYLLGIVQNPNIVNSVVALLSIAGVLVGSGFL
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Pred. No. 2.4e-61;
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APPLICANT: Tian, Hui
APPLICANT: Schultz, Joshua
APPLICANT: Schultz, Joshua
APPLICANT: Schultz, Inc.
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Sitosterolemia Susceptibility Gen
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT APPLICATION NUMBER: US 60/198,465
PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR APPLICATION NUMBER: US 60/198,465

Gene (SSG):

Compositions

GENERAL INFORMATION:

Sequence 1, Application US/09837992 Patent No. US20020081687A1

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RESULT 8
US-09-989-981A-2
Sequence 2, Application US/09989981A
Publication No. US20030049730A1
GENERAL INFORMATION:
APPLICANT: Hobbs, Helen H.
APPLICANT: Shan, Be1
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SEQ ID NO 1
LENGTH: 652
TYPE: PRT
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PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
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OTHER INFORMATION: mouse sitosterolemia susceptibility gene
OTHER INFORMATION: amino acid sequence
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                                                                                                                                                                                                                                                      ---YGL---NETCGGSNTSML-----NHFMCAITQGVQFIEKTCPGATSRFTANFLILY 629
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Best Local :
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PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Tularik Inc.
APPLICANT: Board of Regents, The University of Texas
APPLICANT: Board of Regents, The University of Texas
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
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                                                                                                                                                                                                                                  480 TVIFSSVCYWTLGLYPEVARF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 19.6%; Score 688.5; DB 11; al Similarity 28.1%; Pred. No. 1.7e-60; 188; Conservative 125; Mismatches 233;
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                                                                                                                       RRTYKMPLGNLTIAVSGDKILSAMELDSYPLYAI-----
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                                                     GLSGGFMVL
                                                                                  ---YGL---NETCGGSNTSML-----NHPMCAITQGVQFIEKTCPGATSRFTANFLILY
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LENGTH: 657
TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity
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TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
CURRENT FILING DATE: 2001-08-30
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PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
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AMELDSYPLYAIYLIVIGLSGGFMVLYYVSLRFIKQ 667
                                                                                                                                                                                       SVSAVELFVVEKKLFIHEYISGYYRVSSYFFGKVMSDLLPMRFLPSVIFTCILYFMLGLK
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                                                    IGPWLSWLQYFSIPRYGFTALQYNEFLGQEF-CPGFNVTDNSTCVNSYAICTGNEYLINQ
                                                                                    LWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLT-----IAVSGDKIL--S
                                                                                                                      KTVDAFFIMMFTLIMVAYTASSMALAIATGQSVVSVATLLMTIAFVFMMLFSGLLVNLRT
                                                                                                                                                    PGLQPFLLHFLLVWLVVFCCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSS
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Pred. No. 3.4e-58;
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US-10-108-605-245
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LENGTH: 663
TYPE: PRT
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CURRENT FILING DATE: 2002-03-27
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
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TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
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NUMBER OF SEQ ID NOS: 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-NMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKNYCGVAYPGELLAVMSSSGAGKTTLLNALAFRSPQGIQVSPSGMRLLNGQPVDAKENQ
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                                                                    ALSVGPPVIIPFLLFGGFFLNSGSVPVYLKWLSYLSWFRYANEGLLINQWADVEPGEISC
                                                                                                                                                                                 GELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALAAAALLPTFHM 558
                                                                                                                                                                                                                                                          GSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELEDGLYTTGPYFFAKIL 498
                                                                                                                                                                                                                                                                                                                                TNCLPSP----TKMPGAVQQFTTLIRRQISNDFRDLPTLLIHGAEACLMSMTIGFLYFGH 438
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                                 PLGNLTIAVSGDKILSAMELDSYPLYAIYLIVIGLSGGFWVLYYVSLR 663
                                                                                                                                            AELPLFLTVPLVFTAIAYPMIGLRAGVLHFFNCLALVTLVANVSTSFGYLISCASSSTSM
                                                                                                                                                                                                                      QLTQVGVMNINGAIFLFLTNMTFQNVFATINVFTSELPVFMREARSRLYRCDTYFLGKTI 488
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                                                                                                         ASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCFEGLMKIQFS---RRTYKM 615
                                                                                                                                                                                                                                                                                               -----QPENGYTYKATWFMQFRAVLWRSWLSVLKEPLLVKVRLIQTTMVAILIGLIFLGQ
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o. US20020160934A1
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CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 35
LENGTH: 655
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TITLE OF INVENTION: GENES EXPRESSED IN COLON
FILE REFERENCE: PA-0038 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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              LYAIYLIVIGLSGGFMVLYYVSLRFIKQ |: :: : |: |: | |: |: |: |: |: |
                                                                   WLQYFSIPRYGFTALQHNEFLGQNF-CPGLNATGNNPCNYATCTGEEYLVKQGIDLSPWG
                                                                                                                                               FVMMFTLMMVAYSASSMALATAAGQSVVSVATLLMTTCFVFMMTFSGLLVNLTTTASWLS
                                                                                                                                                                                                                             LFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLPMRMLPSIIFTCIVYFMLGLKPKADAF
                                                                                                                                                                                                                                                                                                         QIIVTVVLGLVIGAIYFGLKNDSTGIQNRAGVLFFL-----TTNQCFSSVSAVE
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                                                                                                        WISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLT-----IAVSGDKIL--SAMELDSYP
                                                                                                                                                                                      LLHFLLVWLVVFCCRIMALAAALLLPTFHWASFFSNALYNSFYLAGGFMINLSSLWTVPA
                                                                                                                                                                                                                                                                  ----ERAMLYYELEDGLYTTGPYFFAKILGE-LPEHCAYIIIYGMPTYWLANLRPGLQPF
                                                                                                                                                                                                                                                                                                                                                HGAEACLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYS-----
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Pred. No. 8e-56;
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US-10-120-687-61
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US-10-120-687-61
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CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US60/169082
PRIOR FILING DATE: 1999-12-06
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TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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PRIOR APPLICATION NUMBER: US 09/731261
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LLHFLLVWLVVFCCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPA
                                         LFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLPMRMLPSIIFTCIVYFMLGLKPKADAF
                                                                         ----ERAMLYYELEDGLYTTGPYFFAKILGE-LPEHCAYIIIYGMPTYWLANLRPGLQPF
                                                                                                                      QIIVTVVLGLVIGAIYFGLKNDSTGIQNRAGVLFFL
                                                                                                                                                         HGAEACLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYS-----
                                                                                                                                                                                                LHQLSGGEKKKKITVFKEISYTTSFC------HQLRWVSKRSFKNLLGNPQASIA
                                                                                                                                                                                                                                   ------DLDEDTCVESSVTPLDTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPTLLI
                                                                                                                                                                                                                                                                                                                   PADFYVDLTSIDRR----SREQELATRE--KAQSLAALFLEKVRDL--DDFLWKAETK--
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                                                                                                                                                                                                                                                                                                                                                                                               RLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRPANF--KCNSGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CRKPVEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGL-SGDVLINGA 111
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Pred. No. 8e
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; ORGANISM: Homo sapiens US-09-961-086-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DOYLE, L. Austin
APPLICANT: ABRUZZO, Lynne
TITLE OF INVENTION: BREAST CANCER RESISTANCE PROTEIN (BCRP) AND THE DNA
TITLE OF INVENTION: WHICH ENCODES IT
FILE REFERENCE: EP19376-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/073,763 PRIOR FILING DATE: 1998-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/961,086
CURRENT FILING DATE: 2001-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US99/02577
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TYPE: PRT
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  QIIVTVVLGLVIGAIYFGLKNDSTGIQNRAGVLFFL---
                                                                                                                                                                                                                                                                                                                                       LDKVADSKVGTQFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCQNSCELGI-QNLSFKVRSGQMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTNG-----FPATASNDLKAFTEGA--VLSFHNICYRVKLKSGF-----LP----
                                                                                      LHQLSGGEKKKKITVFKEISYTTSFC-
                                                                                                                                                                                                           PADFYVDLTSIDRR----SREQELATRE--KAQSLAALFLEKVRDL--DDFLWKAETK--
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                                                                                                                                                                                                                                                                                                                                                                             LRQCADTRYGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLS 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CRKPYEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGL-SGDVLINGA 111
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                                          HGAEACLMSMTIGFLYFGHGSIQLSEMDTAALLEMIGALIPFNVILDVISKCYS-----
                                                                                                                            -----DLDEDTCVESSVTPLDTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPTLLI
                                                                                                                                                                      PADFFLDIINGDSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYK-ETKAE
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                                                                                 -----HQLRWVSKRSFKNLLGNPQASIA
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TTNOCFSSVSAVE 446
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-02ICIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 655
TYPE: PRT
ORGANISM: Homo:
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PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
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             421 GAEACLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYS-----
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                                                                                                                                                                                                                                                                                                           SSPOLVRKC-VAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRL 197
                                                                                                                                                                   ADFYVDLTSIDRR----SREQELATRE--KAQSLAALFLEKVRDL--DDFLWKABTK----
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                                                           HQLSGGEKKKKITVFKEISYTTSFC----
                                                                                                                                         ADFFLDIINGDSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYK-ETKAEL
                                                                                                                                                                                                                                                                                                                                                                                               RPANF -- KCNSGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIEELGL 170
                                                                                               -----DLDEDTCVESSVTPLDTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPTLLIH 420
                                                                                                                                                                                                                                                                   LAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNP 317
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Pred. No. 2e-55;
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                                                       -HQLRWVSKRSFKNLLGNPQASIAQ 398
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	420 398	DLDEDTCVESSYTPLDTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPTLLIH	
····	366 349	ADFYVDLTSIDRRSREQELATREKAQSLAALFLEKVRDLDDFLWKAETK	Qy 318 Db 291
	317 290	LAKGNRLVLISLHOPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCDRYSNP:: :: :	ду 258 рь 231
	257 230	RQCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSR;	Оу 198 Оъ 171
· •	197 170	SSPOLVRRC-VAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRL	Db 113
	138 112		Qy 8 Db 5
	17;	ch 18.2%; Score 638.5; DB 15; Length 655; 11 Similarity 27.9%; Pred. No. 2e-55; 175; Conservative 131; Mismatches 254; Indels 67; Gaps	Query Match Best Local Matches 17
		1: 655 PRT SM: Homo sapiens 455-5	ENGTH: CPE: PI RGANISI
		APPLICATION NUMBER: US/10/090,455 FILING DATE: 2002-03-01 PF SEQ ID NOS: 17 P: FastSEQ for Windows Version 4.0	CURRENT A CURRENT F NUMBER OF SOFTWARE: SEO ID NO
		CANT: Chen, Hongyun CANT: Chen, Hongyun CONT: Le Bihan, Stephane CONT: LE Bihan, Stephane CONTION: NOVEL ABCG4 TRANSPORTER AND USES THEREOF REFERENCE: 100103,406	APPLICANT: APPLICANT: TITLE OF IN
		SULT 15 :-10-090-455-5 Sequence 5, Application US/10090455 Publication No. US20030027259A1 GENERAL INFORMATION.	RESULT 15 US-10-090-455- Sequence 5, Publication GENERAL INFO
-		627 WKNHVALACMIVIFLTIAYLKLLFLKK 653	Db 45
	640 626	ISKVSFLKWCFEGLMKIQPSRRTYKMPLGNLTIAVSGDKILSAMELDSYPL	
	589 567	LHELLVWLVVFCCRIMALAAAALLPTFHMASFESNALYNSFYLAGGFMINLSSLWTVPAW::::::::::::::::::::::::::::::::::::	
····	529 507	474ERAMLYYELEDGLYTTGPYEFAKILGE-LPEHCAYIIIYGMPTYWLANLRPGLQPFL :	Oy 4 Db 4
	447	IIVTVVLGLVIGAIYFGLKNDSTGIQNRAGVLFFLTTNQCFSSVSAVEL	Db 3

Db	Qy	Db ·	Qy	Db	Qy
627 WKNHVALACMIVIFLTIAYLKLLFLKK 653	641 YAIYLIVIGLSGCEMVLYYVSLREIKQ 667	568 LQYFSIPRYGFTALQHNEFLGONF-CPGLNATGNNPCNYATCTGEEYLVKQGIDLSPWGL 626	590 ISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVSGDKILSAMELDSYPL 640	508 VMMFTLMVVAYSASSMALAIAAGQSVVSVATLLMTICFVFMMIFSGLLVNLTTIASMLSW 567	530 LHELLVWLVVECCRIMALAAAALLPTEHMASEESNALYNSEYLAGGEMINLSSLWTVPAW 589

Search completed: July 25, 2003, 17:23:59 Job time: 57 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                 WHIT_DROME
YOH5_YEAST
ABG2_HUMAN
WHIT_ANOGA
WHIT_CERCA
ABG1_MOUSE
WHIT_LUCCU
ABG1_HUMAN
YPC3_CAEEL
WHIT_ANOAL
ABG4_HUMAN
ADP1_YEAST
SCRT_DROME
YOSC_CAEEL
PORA_YEAST
BROW_DROWI
CDR2_CANAL
CDR4_CANAL
CDR4_CANAL
CDR4_CANAL
CDR4_CANAL
YN99_YEAST
CDR3_CANAL
YN99_YEAST
CDR3_CANAL
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SNQ2_YEAST
CDR3_CANAL
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SNG2_CANAL

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Q08234 saccharomyc
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	P14788	P56344	P54933	P38045				P55604	P37624	P73450	P40550	Q02785	
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ALIGNMENTS

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REDIEW. MEDLINE-21474438; PubMed-11590207; Schmitz G., Langmann T., Heimerl S.; "Role of ABCG1 and other ABCG family members in lipid metabolism."; J. Lipid Res. 42:1513-1520(2001). -i- FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the entercytes and in the selective sterol excretion by the liver into bile. -i- SUBUNIT: May form heterodimers with ABCG5 or be tightly coupled to excretion. -i- SUBCELLULAR LOCATION: Integral membrane protein (Probable). Fent-Alternative products: Event-Alternative splicing; Named isoforms-2; Name-1; IsoId-Q9H221-1; Sequence-Displayed;		G8_HUMAN G8_HUMAN ABG8_HUMAN ABG8_HUMAN ABG8_HUMAN STANDARD; PRT; 673 AA. O9H2ZL; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) ATP-binding cassette, sub-family G, member 8 (Sterolin-2). ABCG8. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606; [1] SEQUENCE FROM N.A., VARIANTS SITOSTEROLEMIA THR-231; GLN-263; AND ARG-596, AND VARIANT CYS-54. AEDLINE-2053648; PubMed-11099417; Berge K.E., Tian H., Graf G.A., Yu L., Grishin N.V., Schultz; Kwiterovich P., Shan B., Barnes R., Hobbs H.H.; "Accumulation of dietary cholesterol in sitosterolomia caused"

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99999999999999999999999999999999999
                                                                                                                                                                                                                                                          ProDom; PD000006; ABC_transporter; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Glycoprotein; Transmembrane; Transport; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
             VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: Seems to have a defective ATP-binding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human tissues.

DISEASE: Defects in ABCG8 are a cause of sitosterolemia DISEASE: Defects in ABCG8 are a cause of sitosterolemia or shellfish [MIM:210250]; also known as phytosterolemia or shellfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Strongly expressed in the liver, lower levels in the small intestine and colon. Detectable in a wide variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            artery disease.

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characterized by increased intestinal absorption of all sterols including cholesterol, plant and shellfish sterols, and decreased biliary excretion of dietary sterols into bile. Sitosterolemia patients have hypercholesterolemia, very high levels of plant sterols in the plasma, and frequently develop tendon and tuberous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                 AF351823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9H221-2; Sequence=VSP_000052;
Note=Minor form detected in approximately 10% of the cDNA
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0005; ABC_tran; 1.
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                                                                                                                                                                                                                                                     Disease mutation
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RX MEDLINE-2108560; Pubmed-1127851;
RR RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RR RAWAI J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RR Alawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RR Alawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,
RR Alawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RR Alawa K., Izawa M., Nishi K., Kiyosawa H., Koodo S., Yamanaka I.,
RR Alawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RR Alawa K., Matsuda H.A., Ashburata S., Casavant T.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RR Kuehl P., Lewis S., Matsuo Y., Karinici P., de Bonaldo M.F.,
RR Schriml I.M., Staubli F., Suchenbare I., Fujita M., Gariboldi M.,
Ru Salaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ru Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Na Hayashtzaki Y.,
                                 TISSUE SPECIFICITY, AND INDUCTION.
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Reviterovich P., Shan B., Barnes R., Hobbs H.H.;
"Accumulation of dletary cholesterol in sitosterolemia caused
mutations in adjacent ABC transporters.";
Science 290:1771-1775(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                       "Functional annotation of a Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Two genes that map to the STSL locus cause sitosterolemia: genomic structure and spectrum of mutations involving sterolin-1 and sterolin-2, encoded by ABCG5 and ABCG8, respectively.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H., Ose L., Stalenhoef A.F.H., Mietinnen T., Bjorkhem I., Bruc Pandya A., Brewer H.B. Jr., Salen G., Dean M., Srivastava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21344600; PubMed=11452359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABCG8.
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Last annotation update)
sub-family G, member 8
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                                                                                                                                                                                  full-length mouse cDNA collection.";
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Sciurognathi; Muridae; Murinae; Mus
of the dietary chol
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hem I., Bruckert
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ckert E.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                     SEQUENCE
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InterPro; IPR003439; ABC_transporter
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EMBL; AK004871; BAB23630.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: Seems to have a defective ATP-binding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the liver X receptor SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCTION: Upregulated by cholesterol feeding. Possibly mediated by the liver X receptor/retinoide X receptor (LXR/RXR) pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in the intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: May form heterodimers with ABCG5 or be ABCG5 along a pathway regulating diatery-sterol excretion (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             level,
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een the Swiss Institute of Bioinformatics
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                                                                                                                               60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9DBM0-2;
                                                                                                                                                                                                                                                   Similarity
                                          GRGHGGKIKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTF
                                                                                        MAEKTKEETQLWNGTVLQDASQGLQDSLFSSESDNSLYFTYSGQSNTLEVRDLTYQVDIA
                                                                                                                                                                             MAGKAAEERGLPKGATPQDTS-GLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLA
                        GRGHGGKMKSGQIWINGQPSTPQLVRKCVAHVRQHDQLLPNLTVRETLAFIAQMRLPRTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABC_tran;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABC_transporter; 1.
ABC_TRANSPORTER_1; 1.
ABC_TRANSPORTER_2; 1.
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                                                                                                                                                                                                                                                 81.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence=VSP_000053;
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                                                                                                                                                                                                                              Score 2873; DB 1;
Pred. No. 1.7e-208;
52; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                    4 (POTENTIAL).
CYTOPLASMIC (PC
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .)
Missing (in isoform 2).
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6 (POTENTIAL).
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3 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                 /FTId=VSP_000053.
78012611A5DF2589 CRC64;
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                                                                                                                                               SEQUENCE ENCLOSED STRAIN-Sprague-Dawley;
STRAIN-Sprague-Dawley;
MEDLINE-21344600; PubMed-11452359;
Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H.,
Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H.,
Ose L., Stalenhoef A.F.H., Mietinnen T., Bjorkhem I., Bruc
Ose L., Stalenhoef A.F.H., Mietinnen G., Dean M., Srivastava
                                                                           "Two genes that map to the STSL locus cause sitosterolemia: genc structure and spectrum of mutations involving sterolin-1 and sterolin-2, encoded by ABCG5 and ABCG8, respectively.";

Am. J. Hum. Genet. 69:278-290(2001).

1. FUNCTION: Transporter that appears to play an indispensable in the selective transport of the dietary cholesterol in and of the enterocytes and in the selective sterol excretion by liver into bile.
                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                       ABG8_RAT
P58428;
                                                                      -
                                                                                                                                                                                                                                                                                  ATP-binding
                                                                                                                                                                                                                                                                                           28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                   NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                               28-FEB-2003
                                              SUBUNIT: May form heterodimers with ABCG5 or be ABCG5 along a pathway regulating diatery-sterol excretion (By similarity).
                              SUBCELLULAR LOCATION: Integral ALTERNATIVE PRODUCTS:
                     Event-Alternative
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   IsoId=P58428-1;
                                                                                                                                                                                                                                                                                                                                                                                            VSLRFIKQKPSQDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWC
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
cassette, sub-family G, member 8
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  Sequence=Displayed
                     splicing; Named
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Bruckert E.,
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ProDom; PD000000
SMART; SM00382;
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InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for com
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Note=No experimental confirmation available;
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG
SUBFAMILY.
CAUTION: Seems to have a defective ATP-binding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                             WKAETKOLDEDTCVESSYTPLDTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPTLLIH
                                                                                                                              QVPWFEQLAQFKMPWTSPSCQNSCELGIQNLSFKVRSGQMLAIIGSSGCGRASLLDVITG
                                                                               VQYFTAIGYPCPRYSNPADFYVDLTSIDRRSREQELATREKAQSLAALFLEKVRDLDDFL
                                                                                                                                                                                                                                                                 WKAEAKSLDTGTYAVSQTLTQDTNC-GTAAELPGMIQQFTTLIRRQISNDFRDLPTLFIH
                                                              VQYFTSIGYPCPRYSNPADFYVDLTSIDRRSKEQEVATMEKARLLAALFLEKVQGFDDFL
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Pred. No. 3.2
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MISSING (In Isoform 2):

/FTId=VSP_000054.

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N-LINKED (GLCNAC. . .)
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6 (POTENTIAL).
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STRAIN-Sprague-Davley; TISSUE-Small intestine; MEDLINE-20578753; PubMed-11138003; Lee M.-H., Lu K., Hazard S., Yu H., Shulenin S Allikmets R., Sakuma N., Pegoraro R., Srivasta Dean M., Patel S.B.; "Identification of a gene, ABCG5, important in dietary cholesterol absorption.";
     PROSITE: PS00211; ABC_TRANSPORTER_1; 1. PROSITE: PS50893; ABC_TRANSPORTER_2; 1. ATP-binding: Glycoprotein: Transmembrane:
                                      Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter;
SMART; SM00382; AAA; 1.
                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                      InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter
                                                                                                EMBL; AF312714; AAG53098.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                     Genet. 27:79-83(2001).
FUNCTION: Transporter that appears in the selective transport of the dof the enterocytes and in the select
                                                                                                                                                                                                                      SUBCELLULAR LOCATION SIMILARITY: BELONGS
                                                                                                                                                                                                                                           liver into bile.
SUBUNIT: May form heterodimers with ABCG8 or be ABCG8 along a pathway regulating diatery-sterol excretion (By similarity).
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cassette, sub-family G, member 5
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selective sterol excretion by the
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                                                                                                              FMINLSSLWTVPAWISKVSFLRWCFEGLMKIQF
                                                                                                                                                         LVWLVVFCCRIMALAAAALLPTFHMASFFSNAL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGEVFVNGCELRRDQFQDCVSYLLQSDVFLSSLTVRETLRYTAMLAL-RSSSADFYDKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRV
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 (Rel. 41, (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592
652 AA;
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                                   STANDARD;
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                                                                                                                                  -GYFSAALLAPHLIGEFLTLVLLGMVQNPNIVNSIVALLSISGLLIGSG
Created)
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30.0%;
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 sequence
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                                 PRT;
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update;
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.6e-46;
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use by modified
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sterolin-2, encoded by ABCG5 and ABCG8, respectively.",
Am. J. Hum. Genet. 69:278-290(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitz G., Langmann T., Heimerl S., "Role of ABCG1 and other ABCG family members J. Lipid Res. 42:1513-1520(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20578753; PubMed=11138003; Lee M.-H., Lu K., Hazard S., Yu H., Stallikmets R., Sakuma N., Pegoraro R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SER-550, AND VARIANT GLU-604.
MEDLINE-21344600; PubMed-11452359;
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*Accumulation of dietary cholesterol in sitosterolemia mutations in adjacent ABC transporters.*;

Science 290:1771-1775(2000).
                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "TWO genes that map to the STSL locus cause sitosterolemia: structure and spectrum of mutations involving sterolin-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patel S.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21474438; PubMed-11590207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of a gene, ABCG5, dietary cholesterol absorption."; Nat. Genet. 27:79-83(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dean M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS SITOSTEROLEMIA GLN-146; HIS-389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berge K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20553648; PubMed-11099417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT GLU-604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding
                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Excuropean Bioinformatics Institute. There are no restr
                                                                                                                                                                                DISEASE: Defects in ABGGS are a cause of sitosterolemia (MIM:210250); also known as phytosterolemia or shellfish sterolemia. It is a rare autosomal recessive disorder characterized by increased intestinal absorption of all sterols including cholesterol, plant and shellfish sterols, and decreased biliary excretion of dietary sterols into bile. Sitosterolemia patients have hypercholesterolemia, very high levels of plant sterols in the plasma, and frequently develop tendon and tuberous xanthomas, accelerated atherosclerosis and premature coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the entercytes and in the selective sterol excretion by the
                                                                                                                                            artery disease.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Strongly expr
in the small intestine and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver into bile. SUBUNIT: May for
                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABCG8 along a pathway regulating
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    non-profit and this st
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                        institutions
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sub-family G, member 5 (Sterolin-1).
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  not removed.
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                 as long
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                                                                                                                                            TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shulenin S.,
., Srivastava
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               ormatics and the EMBL outst
There are no restrictions
ong as its content is in
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bbs H.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                       e protein in the li
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Usage
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                                                                                                                                                                                                                                                                                                                                                                                                     the liver,
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A.K., S
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  and for
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                                                                              collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000006;
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Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0030299; P:cholesterol absorption;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew;
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                                                                                                                                                                                                                  Similarity
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                LSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRY
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| VELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEH
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                                                                                                             NGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAE
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AAG53099.1;
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28.9%;
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                                                                                                                                                                                                         124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Transport; Polymorphism;
                                                                                                                                                                                                                Score
Pred.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
E -> Q (in sitosterolemia).
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R -> H (in sitosterolemia).
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950BABFCBB6A1536
                                                                                                                                                                                                                                                                        R -> S (in sitosterolemia)
/FTId=VAR_012248.
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R -> H (in_sitosterolemia).
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RESULT ABGS_MARCH PROCESSOR OF THE PROCE
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                                                                                                                                                                                                                                                                                                  ***Berge K.E., Tian H., Graf G.A., Yu L., Grishin N.V., Schultz J., Kwiterovich P., Shan B., Barnes R., Hobbs H.H.;

***Accumulation of dietary cholesterol in sitosterolemia caused by mutations in adjacent ABC transporters.**;

**Science 290:1771-1775(2000).

-i- FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out liver into bile.

-i- SUBUNITY. Loc. **

-
                                          This SWI
between
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28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a gene, ABCG5, dietary cholesterol absorption."; Nat. Genet. 27:79-83(2001).
                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-20578753; PubMed-11138003;
Lee M.-H., Lu K., Hazard S., Yu H., St
Allikmets R., Sakuma N., Pegoraro R.,
Dean M., Patel S.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                          ABCG8 along a pathway regulating diatery-sterol absorption and excretion (By similarity).

SUBCELULAR LOCATION: Integral membrane protein (Probable).

TISSUE SPECIFICITY: Expressed in the intestine and, at lower level, in the liver.

INDUCTION: Upregulated by cholesterol feeding. Possibly mediated by the liver X receptor/retinoic X receptor (LXB/RXR) pathway.

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                       SUBUNIT: May form heterodimers with ABCG8 or
        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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(Rel. 41, Last annotation update)
cassette, sub-family G, member 5 (Sterolin-1).
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Rodentia;
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SEQUENCE
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SMART; SM00382; AAA;
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N-LINKED (GLCNAC...)
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RESULT
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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botochan M.R., Bouck J., Brokstein P., Brottier P.,

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RA Borkova D., Botochan M.R., Bouck J., Brokstein P., Brottier S.M.,

RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Junkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Bownes M., Dugan-Rocha S., Fleischmann W.,

RA Dodson K., Doup F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Dodson K., Doup F., Borrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Ralush F., Karpen G.H., Ke Z., Kunnison J.A., Ketchum K.A.,

RA Harris N., Mattel B., Kolltosh T.C., McL
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Lasko P., Lei Y., Levitsay ......
Liu X., Mattei B., McIntosh T.C., McLeoc
Merkulov G., Milshina N.V., Mobarry C.,
Merkulov B., Murphy L
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W OR EG:BACN33B1.1 OR CG2759.
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01-MAR-1989 (Rel. 10, Created)
01-NOV-1991 (Rel. 20, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Dual-tagging gene trap of novel genes in Drosophila melanogaster."; Genetics 157:727-742(2001).
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MEDLINE=21100348; PubMed=11156992;
Lukacsovich T., Asztalos Z., Awano
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MEDLINE-2196011; PubMed-10731137;

Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,

Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu F.

Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova

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Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,

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Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                  EMBL; X51749; CAA36038.1; --
EMBL; X02974; CAA26716.1; --
EMBL; AB028139; BAA78210.1; --
EMBL; AE003425; AAP45826.1; --
EMBL; AL133506; CAE65847.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R. F., Zaveri J.S., Zhan M., Zhang G., Zhang L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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SEQUENCE OF 224-331 FROM N.A.
SEQUENCE OF 224-331 FROM N.A.
MEDLINE-89339145; PubMed-2503416;
Tearle R.G., Belote J.M., McReown M.,
Tearle R.G., Characterization of the s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics 122:595-606(1989).
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY FOR THE TRANSPORT OF PIGMENT PRECURSORS INTO PIGMENT CELLS RESPONSIBLE FOR EYE COLOR. WHITE DIMERIZE WITH BROWN FOR THE TRANSPORT OF GUANINE AND WITH SCARLET FOR THE TRANSPORT OF
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scarlet gene
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Borkova D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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GO; GO:0004888; F:transmembrane receptor activity; NAS GO; GO:0006727; P:ommochrome biosynthesis; IMP. InterPro; IPR003593; ABA_ATPASS. INTERPO; IPR003439; ABC_transporter. InterPro; IPR005284; Pigment_permease. Pfam; PF00005; ABC_tran; 1.

FlyBase;

FBgn0003996; w.

EMBL; X76202; CAA5: PIR; S08635; FYFFW

CAA53795.1;

TIGRFAMs; TIGR00955; 3a01204; SMART; SM00382; AAA;

ABC_TRANSPORTER_1; 1. ABC_TRANSPORTER_2; 1.

PD000006; ABC_transporter;

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                                      TOH5_YEAST STANDARD; PRT; 1294 AA 008234; Q08233; 01-NOV-1997 (Rel. 35, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Probable ATP-dependent transporter YOL074C/YOL074C/YOL075C.
                                                                                                                    YEAST
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                         Saccharomyces cerevisiae (Baker's yeast).
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NP_BIND
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         ota; Fungi;
romycetales;
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                                                                                                                                                        TSSNTTCPSSGKVILETLNFSAADLPLDYVGLAILIVSFRVLAYLALR 680
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                                                                                                                                                                                                                                                                                        QLTQVGVMNINGAIFLFLTNMTFQNVFATINVFTSELPVFMREARSRLYRCDTYFLGKTI
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                                                                                                                                                                                                                                                                  GELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALAAALLPTFHM
                                                                                                                                                                                                                                                                                                                                                                           LAV----VPGREIESRDRIAKICDNFAISKVARDMEQLL---ATKNLEK------PLE
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     Ascomycota; Saccharor; Saccharomycetaceae;
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ATP (BY SIMILARITY).
              Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 656; DB 1;
Pred. No. 1.2e-41;
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                                                YOL074C/YOL075C.
                                                                                                      1294 AA
    Saccharomyces
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Matches 171
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tzermia M., Katsoulou C., Alexandraki D.;
"Sequence analysis of a.33.2 kb segment from the left arr
chromosome XV reveals eight known genes and ten new open
frames including homologues of ABC transporters, inosito;
phosphatases and human expressed sequence tags.";
Yeast 13:583-589(1997).
                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000006; ABC_transporter; SMART; SM00382; AAA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003593; AAA ATPASE.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 2.
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SGD; S0005435; YOL075C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 274817; CAA99085.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                               105
                                                                                                                       45
                                                                                                                                                                           Similarity
TAHNLYKTLSRLAK-GNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFT: | ::|| | | | | ::: | :| : | | : : | |
                                MVEQLIEELGIKDCADTLVGDNSHRGLSGGEKRRLSIGTQMISNPSIMFLDEPTTGLDAY
                                          PKRAHLDGQ-DHPIQKHVIMAYLPQQDVLSPRLTCRETLKFAADLKL----NSSERTKKL
                                                                                                                     VNTFSMDLPSGSVMAVMGGGSGKTTLLNVLASKISGGLTHNGSIRYVLEDTGSEPNETE
                                                                                                                                 IQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGRGHGGKIKSGQI---
                                                                                                ----WINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKR-
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1062
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ABC_TRANSPORTER_2;
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551
625
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Pred. No. 4.4e-41;
L1; Mismatches 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the left arm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                    Length 1294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9UNQO: O95374; Q9BY73; Q9NUSO;
16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP-binding cassette, sub-family G, member 2
                                                                                                                                                                                                                                                                                                  MEDLINE-99065313; PubMed-9850061;
Allikmets R., Schriml L.M., Hutchinson A., Romano-Spica
"A human placenta-specific ATP-binding cassette gene (AF
chromosome 4922 that is involved in multidrug resistance
                                                                     Kage K., Tsu
Sugimoto Y.;
                                                                                                                                            Doyle L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                          binding cassette transporter) (Breast cancer ABCG2 OR ABCP OR BCRP OR BCRP1.
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                Ross D.D.;
                                                                                                                                                        ERRATUM.
                                                                                                                                                                                                                                                                                             Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
        SEQUENCE OF 198-655 FROM N.A.
                                  Submitted
                                                       Breast cancer resistance protein
                                                                                                                    roc. Natl.
                                                                                                                                                                                 Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                     multidrug resistance transporter from human MCF-7
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                                                                               Tsukahara
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                              (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                    Acad.
                                                                                                                                          Yang W., Abruzzo L.V.,
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Primates;
                                                                               Sugiyama
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*Role of ABCG1 and other ABCG family members in lipid metabolism.*;

J. Lipid Res. 42:1513-1520(2001).

-I- FUNCTION: XENOBIOTIC TRANSPORTER THAT APPEARS TO PLAY A MAJOR ROLE
IN THE MULTIDRUG RESISTANCE PHENOTYPE OF A SPECIFIC MCF-7 BREAST
CANCER CELL LINE. MHEN OVEREXPRESSED, THE TRANSFECTED CELLS BECOME
RESISTANT TO MITOXANTRONE, DAUGNORUBICIN AND DOXORUBICIN, DISPLAY
DIMINISHED INFRACELLULAR ACCUMULATION OF DAUGNORUBICIN, AND
MANIFEST AN ATP-DEPENDENT INCREASE IN THE EFFLUX OF RHODAMINE 123.

-I- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

-I- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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SMART; SM00382; AAA;
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EMBL; AK002040;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restricted the surpession of the surpes
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                                                                                                                                                                                                                                                                          RANSMEM
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P:small molecule transport;
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F:xenobiotic-transporting
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V -> A (IN REF. 2
E -> Q (IN REF. 2
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Q27256; Q1706;
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
 MEDLINE-96423158; PubMed-8825759;
Besansky N.J., Bedell J.A., Beneds
                                                                                                                      Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Ano
NCBI_TaxID-7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                 White protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                       YAIYLIVIGLSGGFMVLYYVSLRFIKQ 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQYFSIPRYGFTALQHNEFLGQNF-CPGLNATGNNPCNYATCTGEEYLVKQGIDLSPWGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHFLLVWLVVFCCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLPMRMLPSIIFTCIVYFMLGLKPKADAFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DLDEDTCVESSVTPLDTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPTLLIH 420
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. 35, Last sequ
. 40, Last anno
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482 R
72343 MW;
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27.9%;
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                          Benedict M.Q.,
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MISSING (IN REF. 5
R -> T (IN REF. 2)
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Pred. No. 1.
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                                                                                                                                   Nematocera; Culicoidea; Anopheles.
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                        Mukabayire 0.,
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Best Local S
Matches 189
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TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insect Mol. Biol. 4:217-231(1995).

-I- FUNCTION: MAY BE PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY FOR THE TRANSPORT OF PIGMENT PRECURSORS INTO PIGMENT CELLS RESPONSIBLE FOR EYE COLOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR005284; Pigment_permease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                         307
                                                                            276
                                                                                                                247
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     336
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                                                         IFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDLTSIDRRSREQE
                                                                                                                               GERRRYSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRLVLISLHQPRSD
                                                                                                                                                                                                           LLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQCADTRVGNM-YVRGLSG
                                                                                                                                                                                                                                                   PS00211; ABC_TRANSPORTER_1; 1. PS50893; ABC_TRANSPORTER_2; 1. ATP-binding; Transmembrane; Transport.
LATREKAQSLAALFLEKVRDLDDFLWKAETKDLDEDTCVESSVTPLDTNCLPSPT
                                                                                                                                                                                                                                                                                           QMLAIIGSSGCGRASLLDVITGRGHGG-KIKSGQI-WINGQPSSPQLVRKCVAHVRQHNQ
                                                                                                                                                                                                                                                                                                                               RLT---YTWKEIDVFGEAPTDGKPREPLCTRLRNCCTRQRKDFNPRKHLLKNVTGVAKSG
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                                  LYCLFDKILLVAEGRVAFLGSPYQSAEFFSQLGIPCPPNYNPADFYVQMLAIAPAK----
                                                                                                          GERKRLAFASETLTDPHLLLCDEPTSGLDSFMAHSVLQVLKGMAMKGKTIILTIHQPSSE
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Pred. No. 1.8e-39;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N -> S (IN REF 1; AAC47423).
SRS -> YAR (IN REF 1; AAC47423).
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                                             PROSITE;
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 ProDom; PD000000
SMART; SM00382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Tephritoidea; Tephritidae; Ceratitis.

NCBI_TaxID=7313;
                                                                   SMART; SM00382; AAA; 1.
TIGRFAMs; TIGR00955; 3a01204; 1.
                                                                                                           Pfam; PF00005; ABC_tran;
                                                                                                                                                               EMBL; x89933; CAA61998.1;
                                                                                                                                     InterPro;
                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                               Zwiebel L.J., Saccone G., Zacharopoulou A., Besansky N.J., Favia G., Collins F.H., Louis C., Kafatos F.C.; The white gene of Ceratitis capitata: a phenotypic marker
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-96123276; PubMed-8533095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHIT_CERCA
Q17320;
                                                                                                                           interPro;
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01-NOV-1997 (Rel.
16-OCT-2001 (Rel.
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PS00211; ABC_TRANSPORTER_1; 1.
PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Transmembrane; Transport.
121 128 ATP (BY SIMILARITY).
1427 445 POTENTIAL.
                                                                                          PD000006; ABC_transporter; 1.
                                                                                                                  IPR003593; AAA_ATPase.
IPR003439; ABC_transporter.
IPR005284; Pigment_permease.
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WADVKPGEITCTLSNTTCPSSGEVILETLNFSASDLPFDFIGLALLIVGFRISAYIAL
                      FS---RRTYKMPLGNLTIAVSGDKILSAMELDSYPLYAIYLIVIGLSGGFMVLYYVSL
                                            LISCACSSTSMALSVGPPVIIPFLLFGGFFLNSGSVPVYFKWLSYLSWFRYANEGLLINQ
                                                           AAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCFEGLMKIQ 607
                                                                                        RCDTYFLGKTIAELPLFLVVPFLFTAIAYPLIGLRPGVDHFFTALALVTLVANVSTSFGY 553
                                                                                                              TTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMAL 547
                                                                                                                                    AVLIGLIFLGQQLTQVGVMNINGAIFLFLTNMTFQNSFATITVFTTELPVFMRETRSRLY
                                                                                                                                                           SMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELEDGLY
                                                                                                                                                                                                                              LAVVPGREVESRDRVAKICDNFAVGKVSREMEQNFQKLVKSNGFGKEDENEYTYKASW--
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POTENTIAL.
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Pred. No. 3.2e-39;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                   ------FMQFRAVLWRSWLSVLKEPLLVKVRLLQTTMV
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ABGILT 12
ABGILMOUSE
ID ABGIL
AC 06434
AC 06434
AC 06434
AC 07 01-NO
DT 01-NO
DT 28-FE
DE ATP-b
DE (ATP-b
GN ABGGI
OS MUS m
OC EUKAR
OC Mamma
OX NCBI
RN (11)
RP SEQUE
RA SEQUE
RA CCROOP
RA GCROOP
RA AGGILD
RA CCROOP
RA GCROOP
RA GOLDE
SEQUENCE FROM N.A.
MEDLINE-97186700; PubMed-9034316;
Croop J.M., Tiller G.E., Fletcher
Goldenson D., Son D., Arciniegas S
                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP-binding cassette, sub-family G, member 1
(ATP-binding cassette transporter 8).
ABCG1 OR ABC8 OR WHT1.
                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                            ABG1_MOUSE
Q64343;
                                                                                                                                                                                                                                                                             MOUSE
                                                                                NCBI_TaxID=10090;
                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                         STANDARD;
                                                                                               Chordata;
Rodentia;
                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                  J.A.,
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              M.L.,
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                Raab
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MGD; MGI:107704; Abcg1.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR005284; Pigment_permease.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
                                          PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Transmembrane; Transport.
                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                 TIGREAMS; TIGRO0955;
                                                                                              ProDom; PD00000
SMART; SM00382;
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"Role of ABCG1 and other ABCG family members in lipid metabolism.";
J. Lipid Res. 42:1513-1520(2001).
-1- FUNCTION: Transporter involved in macrophage lipid homeostasis. Is an active component of the macrophage lipid export complex. Could also be involved in intracellular lipid transport processes. The role in cellular lipid hemeostasis may not be limited to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human white/murine ABC8 mRNA levels are highly induced in
lipid-loaded macrophages. A transcriptional role for specific
oxysterols.";
                     RANSMEM
                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21474438; PubMed=11590207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venkateswaran A., Repa J.J., Lobaccaro
Mangelsdorf D.J., Edwards P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96359154; PubMed-8703120; Savary S., Denizot F., Luciani M.-F., "Molecular cloning of a mammalian ABC Drosophila white gene";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20261604; PubMed-10799558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic sequence and structure of the human ABCG1 Biochem. Biophys. Res. Commun. 280:121-131(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assmann G., Cullen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 275:14700-14707(2000).
                                                                                                                                                                                                                                                                                                                                                                                           macrophages.
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
TISSUE SPECIFICITY: EXPRESSED MAINLY IN BRAIN, THYMUS, LUNG,
ADRENALS, SPLEEN AND PLACENTA. LITTLE OR NO EXPRESSION IN LIVER,
                                                                                                                                                                                                                                                                                                                                                       INDUCTION: Strongly induced in macrophage cell line during cholesterol influx. Induction is mediated by receptor/retinoide X receptor (LXR/RXR) pathway.
                                                                                                                                                                                                                                                                                                                                          receptor/retinoide x receptor (LXR/RXR) pathway.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                   SUBFAMILY
                                                                                                                                                                                AF323659; AAK27442.1; -.
                                                                                                                                                                                                           034920;
                                                                                                       PD000006; ABC_transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND PROBABLE FUNCTION
                                                                                                                                                                                             AAB47738.1; -. CAA88636.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hite gene.";
7:673-676(1996).
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         414
433
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                                                                                  3a01204; 1
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                       Transport.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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transporter homologous
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01-NOV-1997
16-OCT-2001
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WHIT_LUCCU Q05360;

STANDARD;

PRT;

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A

Eukaryota;

Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly). Eukaryota: Metazoa: Arthropoda; Hexapoda; Insecta; Pterygota;

White

(Rel. 31, Created) (Rel. 35, Last seq (Rel. 40, Last ann

Last sequence update)
Last annotation update)

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Matches
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
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IAETCHFQKSEAILRELDVENAKLY-LDFIVLG--
                         LGNLTIAVSGDKILSAMELDSYPLYAIYLIVIGLSGGFMVLYYVSLRFI
                                                                           FSNALYNSFYLAGGFMINLSSLWTVPA---WISKVSFLRWCFEGLMKIQF--SRRTYKMP
                                                                                                         PFQIMEPVAYCSIVYWMTSQPSDAVREVLEAALGTMTSLVAQSLGLLIGAASTSLQVATE
                                                                                                                                   PEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALAAAALLPTFHMASF
                                                                                                                                                            AKKVLSNSGFLFFSMLFLMFAALMPTVLTFPLEMSVFLREHLNYWYSLKAYYLAKTMADV
                                                                                                                                                                                      QLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELEDGLYTTGPYFFAKILGEL
                                                                                                                                                                                                                          SASCL--
                                                                                                                                                                                                                                              DTNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPTLLIHGAEACLMSMTIGFLYFGHGSI
                                                                                                                                                                                                                                                                         ASGEYGDQNSRLVRAVREGMCDADYKRDLGGDTDVNPFLWH---RPAEEDSASMEGCHSF
                                                                                                                                                                                                                                                                                                    TSIDRRSREQELATREKAQSLAALFLEKV---RDLDDFLWKAETKDLDEDTCVESSVTPL
                                                                                                                                                                                                                                                                                                                                                         VLISLHQPRSDIFRLEDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDL
                                                                                                                                                                                                                                                                                                                                                                                    TGS-----LSGGQRKRLAIALELVNNPPVMFFDEPTSGLDSASCFQVVSLMKGLAQGGRS
                                                                                                                                                                                                                                                                                                                                                                                                     ---LKGISGKFNSGELVAIMGPSGAGKSTLMNILAGYRETG--MKGAVLINGMPRDLRCF
                                                    VGPVTAIPVLLFSGFFVSFD---TIPAYLQWMSYISYVRYGFEGVILSIYGLDREDLHCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNN--FTEAORFSSLPRRAAVNIEFKDLSYSV---PEGPWWKKKGYKTL----
                                                                                                                                                                                                                                                                                                                               IVCTIHQPSAKLFELFDQLYVLSQGQCVYRGKVSNLVPYLRDLGLNCPTYHNPADFVMEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQCADTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNSLYFT----YSGQPN----TLEVRDLNYQVDLASQVPWFEQLAQFKMPWTSPSCQNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                          RKYSCYIMQDDMLLPHLTYQEAMMYSAHLKLQE--KDEGRREMYKEILTALGLLPCANTR
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25.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 621;
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 666;
IFFISLRLI
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                                                                              616
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97087158; PubMed-8933176; Garcia R.L., Perkins H.D., Howells A.J.; The structure, sequence and developmental pattern of expression the white gene in the blowfly Lucilia cuprina."; Insect Mol. Biol. 5:251-260(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elizur A., Vacek A.T., Howells A.J.;
"Cloning and characterization of the white and topaz eye color genes from the sheep blowfly Lucilia cuprina.";
J. Mol. Evol. 30:347-358(1991)
                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neoptera; Endopterygota; Calliphoridae; Lucilia.
                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                FIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MAY BE PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM RECESSARY FOR THE TRANSPORT OF PICHENT PRECURSORS INTO PIGMENT CELLS RESPONSIBLE FOR EYE COLOR.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
     325
                              282
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                                                                                                                                                                                                                                                                                                                                                                                        PS00211, ABC_TRANSPORTER_1; 1.
PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Transmembrane; Transport
ATP-126 ATP (POTENTIAL).
                                                                                           G-NMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRL-
                                                                                                                                                VLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDL
                                                                             GVPGRVKGLSGGERKRLAFASEALTDPPLLTCDEPTSGLDSFMAASVVQVLKKLSQRGKT
                                                                                                                                 ARCAYVQQDDLFIGSLTAREHLIFQATVRMPRTMTQKQKLQRVDQVIQDLSLIKCQNTII
                                                                                                                                                                                      IKNVCGVAYPGELLAVMGSSGAGKTTLLNALAFRSARGVQISPSSVRMLNGHPVDAKEMQ
                                                                                                                                                                                                              IQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGR-GHGGKIKSGQI-WINGQPSSPQLVR
TSIDRRSREQELATREKAQSLAALF-LEKV-RDLDDFLWK--AETKDLDEDTCVESSVTP
                         VILTIHOPSSELFELFOKILLMAEGRVAFLGTPVEAVDFFSFIGAOCPTNYNPADFYVOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  00382; AAA;
TIGR00955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003593; AAA_ATPase.
IPR003439; ABC_transporter.
IPR005284; Pigment_permease.
0005; ABC_tran; 1.
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA82057.1;
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                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABC_transporter;
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                                                                                                                                                                                                                                                                                                 75365 MW;
                                                                                                                                                                                                                                                       17.7%;
29.3%;
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                                                                                                                                                                                                                                             119;
                                                                                                                                                                                                                                                        Score 620.5;
Pred. No. 5.4
                                                                                                                                                                                                                                                                                              POTENTIAL.
D16FC11C97EED51D CRC64;
                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                       .4e-39;
                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                            259;
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                                                                                                                                                                                                                                          Indels
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RESULT 14
ABG1_HUMAN
ID ABG1_HI
AC Q9BXL3
DT 01-NOV
DT 28-FEB
DT 15-SEP
DE ATP-b4
DE ATP-b4
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DE ATP-b4
CO HOMO SI
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                                                                                                                                                                                                                                                                                              Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
A Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
A Polley A., Menzel U., Delabar J., Kumpf K., Lehnann R., Patterson D.,
A Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Lehrach H., Reinhardt R., Yaspo M.-L.;
The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG1_HUMAN STANDARD; PRT, P45844; O9BXK6; Q9BXK7; Q9BXK8; Q9BXL3; Q9BXL4; 01-NOV-1995 (Rel. 32, Created) 28-FEB-2003 (Rel. 41, Last sequend 15-SEP-2003 (Rel. 42, Last annotation)
Berry A., Scott H.S., Kudoh J., Talior I., Koros Wattenhofer M., Guipponi M., Barras C., Rossier Wang J., Kawasaki K., Asakawa S., Minoshima S., Antonarakis S.E., Bonne-Tamir B.;
"Refined localization of autosomal recessive nor
                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                  MEDLINE-20408883; PubMed-10950923;
                                                                                                                                                                                                                                                                        Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20289799; PubMed-10830953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perrin G., Antonarakis S.E.;
"Cloning of the cDNA for a human homologue of gene and mapping to chromosome 21q22.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen H.M., Rossier C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-2003 (Rel. 42, Last annotation update) ATP-binding cassette, sub-family G, member 1 (ATP-binding cassette transporter 8).
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Q9BXK9; Q9BXL0;
                                                                                    Korostishevsky M.
nonsyndromic deafness
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MEDLINE-21474438; PubMed-11590207; Schmitz G., Langmann T., Heimerl S.; Role of ABCG1 and other ABCG family members in lipid metabolism."; J. Lipid Res. 42:1513-1520(2001).

1- FUNCTION: Transporter involved in macrophage lipid homeostasis. Is an active component of the macrophage lipid export complex. Could ralso be involved in intracellular lipid transport processes. The role in cellular lipid hemeostasis may not be limited to
                                                                                                                                                                                                                                                                                                                    MEDLINE-2010556; PubMed-10339163;
Klucken J., Buechler C., Orso E., Kapinski W.E.,
Porsch-Oezcueruemez M., Liebisch G., Kapinsky M., Diederich W.,
Porbnik W., Dean M., Allikmets R., Schmitz G.;
"ABCG1 (ABC8), the human homolog of the Drosophila white gene, is
regulator of macrophage cholesterol and phospholipid transport.";
Proc. Natl. Acad. Sci. U.S.A. 97:817-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venkateswaran A., Repa J.J., Lobaccaro J.-M.A.,
Mangelsdorf D.J., Edwards P.A.;
"Human white/murine ABC8 mRNA levels are highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Croop J.M., Tiller G.E., Fletcher J.A., Lux M.L., Raab E., Goldenson D., Arciniegas S., Son D., Wu R.; "Isolation and characterization of a mammalian homolog of the Drosophila white gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porsch-Oezcueruemez M., Langmann T., Heimerl S., Borsukova H., Kaminski W.E., Drobnik W., Honer C., Schumacher C., Schmitz G.; "The zinc finger protein 202 (ZMP202) is a transcriptional repressor of ATP binding cassette transporter Al (ABCA1) and ABCG1 gene expression and a modulator of cellular lipid efflux."; J. Biol. Chem. 276:12427-12433(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipid-loaded macrophages. A transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20261604;
                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION, AND PROBABLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                             oxysterols."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 185:77-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 33-678 FROM N.A. TISSUE-Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lorkowski S., Rust S., Engel Assmann G., Cullen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4; MEDLINE-21092576; PubMed-11162488;
                                                                                                                                                                                                                                                                                                      REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97186700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFNB10 locus using 34 novel microsatellite markers, genomic structure, and exclusion of six known genes in the region.", Genomics 68:22-29(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-21192304; PubMed-11279031;
                                                                                                          macrophages.
SUBUNIT: May form heterodimers with several heterologous of the ABCG subfamily.
SUBCELULAR LOCATION: Integral membrane protein. Predomin localized in the intracellular compartments mainly associ the endoplasmic reticulum (ER) and Golgi membranes.
ALTERNATIVE PRODUCTS:
ALTERNATIVE PRODUCTS:
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                                                  IsoId=P45844-2;
                            ime=3; Synonyms=ABDE;
IsoId=P45844-3; Sequ
                                                                                              Comment-Additional isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence and structure of the human ABCG1 (ABC8) gene.";
Blophys. Res. Commun. 280:121-131(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=9034316;
   Sequence-VSP_000051
                         Sequence=VSP_000048,
                                                 Sequence-VSP_000047,
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                                                                                                        splicing; Named isoforms=7
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EMBL;
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This
                           European Bioinformatics Institute.
                                                                                                                                                                              TISSUE SPECIFICITY: EXPRESSED IN SEVERAL TISSUES.
INDUCTION: Strongly induced in monocyte-derived macrophages during cholesterol influx. Conversely, mRNA and protein expression are suppressed by lipid efflux. Induction is mediated by the liver x
                                                                                                                                            SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                        Name=7; Synonyms=C;
IsoId=P45844-7; S
                                                                                                                           SUBFAMILY.
                                                                                                                                       receptor/retinoide x receptor (LXR/RXR) pathway.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG
                                                                                                                                                                                                                                                                                                                                       Name=6; Synonyms=HI;
IsoId=P45844-6; Se
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                                            SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
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or send an use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement email to license@isb-sib.ch). (See http://www.isb-sib.ch/announce/ a collaboration 8

EMBL; AJ289149; AJ289150; AJ289145; AJ289146; AJ289147; AJ289141; AJ289142; AJ289143; AJ289144; 289148; CAA62631.1; ALT_INIT. AAK2883 BAA95530 AAK288 AAK288 AAK28836 CAC00730 CAC00730 CAC00730 JOINED ALT_INIT. ALT_INIT. ALT_INIT. JOINED. JOINED. JOINED JOINED

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Q11180;
Q1-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
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 Eukaryota; Metazoa; Nemato Rhabditidae; Peloderinae;
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AF323647;
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                                                                                                                                  -IFFISLRLI
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AAK28835.1;

AAK28835.1;

AAK28835.1;

AAK28835.1;

AAK28835.1;

AAK28835.1;
          Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.6%;
                                                                                                                                  665
 Caenorhabditis
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Pred. No. 9.8e-39;
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                                     n update)
chromosome
        Rhabditida; Rhabditoidea;
                                      III.
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2:
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                                                                                                                                                                                                                                                                                           Local
482
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Hypothetical protein;
NP_BIND 27 34
TRANSMEM 336
TRANSMEM 425 445
TRANSMEM 453 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00955; PROSITE; PS00211; ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00005; ABC_tran; 1
ProDom; PD000006; ABC_trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR005284; Pigment_permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U13645; AAA20989.2; WormPep; C05D10.3; CE29170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                !- SUBCELLULAR LOCATION:
!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 VAHVROHNQLLPNLTVRETLAFIAOMRL-PRTFSQAORDKRVEDVIAELRLROCADTRVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 IQNLSFKVRSGQMLAIIGSSGCGRASILDVITGRGHGGKIKSGQIWINGQPSSPQLVRKC : |: | | | | | | |: |: :: :|:
LEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFC
                                        ITGIVFF-----QTPVTPATIISINGIM-FNHIRNMNFMLQFPNVPVITAELPIVLRE
                                                                                                                                                                                                                                                                                                   IITIHQPSSHVYSLFNNVCLMACGRVIYLGPGDQAVPLFEKCGYPCPAYYNPADHLIRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long as and this statement is not removed. U
                                                                                     TIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDV------
                                                                                                                               FVTGSDTS---EKTKTFFNQDYNASFWTQFLALFWRSWLTVIRDPNLLSVRLLQILITAF
                                                                                                                                                                        SYTPLDTNCLPSPTKM------PGAVQQFTTLIRRQISNDFRDLPTLLIHGAEACLMSM
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                                                                                                                                                                                                                                                             SIDRRSREQELATREKAQSLAALFLEKVRDLDDFLWKAETKDLDEDTC-----VES
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BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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ATP (POTENTIAL).
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Pred. No. 1
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POTENTIAL.
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6; Mismatches
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ches 260;
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15;

Search c Job time	DЬ	Qy	DЪ	Qγ	Ďδ	Qy	DЬ
Search completed: July 25, 2003, 17:12:45 Job time : 30 secs	581 GIRIIAYVAL 590	653 GEMVLYYVSL 662	522 ALAINEWDSIKVIPECFNSSMTAFALDSCPKNGHQVLESIDFSASHKIFDI-SILFGMFI 580	602 GLMKIQFSRRTYKNPLGNLTIAVSGDKILSAMELD-SYPLYAIYLIVIGLSG 652	462 AISISYAVATIFANTDVAMTILPIFVVPIMAFGGFFITFDAIPSYFKWLSSLSYFKYGYE 521	FFSNALYNSFYL	402 NANGYYRTSAYFLAKNIAELPQYIILPILYNTIVYWNSGLYPNFWNYCFASLYTILITNV 461

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
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Maximum DB seq length: 2000000000
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Perfect score:
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                        by analysis of the total
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:
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                                                                                                                                                                                                                                                                                                                               score of the result being printed,
                                                                                                                                                                                                                                                                                                                      score distribution
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70	571.5 16	72	10.5	612 17	17	18	20		.5	18	.5 18	.5 18	.5 18	.5 18	.5 18	.5 18	.5 18	.5 18	.5 18	.5 18	56 18	5 19	6 19	9	88.5 19	88.5 19	5 . 19	88.5 19	91.5 1	بر		1	697 19	_	_	
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АВВ99696	AAE28968	ABB99694	ABB64566	AU96991	ABP52126	ABB98349	BB82647	ABB57112	вв07273	AA014783	AA014782	BB07270	BP52127	AAU04348	AY95365	AY15221	AU80029	A014781	AAU80028	AAB60104	ABB59384	AAY78981	ABB07272	ABP52128	AAE31702	AAE13309	AAE13308	AAE13289	AAU96985	AU96992	AAU96989	AAE31704	AAE13290	Ó	AAU96984	
acid s	ABCG4		Drosophila melanog	Human ABCG5 mutant	00	ABC tra	DevG22 ho	ischa			BCRP-	n BCRP (huBCR	S	n BCRP/M	ή.	t Cance	ABCG2	BCRP pro	ABCG2 Ho	Human transport or	Drosophila melanog		(mBCR	sapiens				sitosterola	ABCG5	ABCG5	ABCG5 mutan	ABCGS	sitost	ABCG5	Human ABCG5 protei	

ALIGNMENTS

RESULT 1 AAE31705

24-MAR-2003 (first entry)

Human ABCG8 protein.

AAE31705;

AAE31705 standard; Protein; 673

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(TULA-) TULARIK INC. (TEXA) UNIV TEXAS SYSTEM human; ABCG5. ABC family cholesterol transporter; ABCG8; sterol-related disorder; sitosterolaemia; hyperlipidaemia; hypercholesterolaemia; gall stone; HDL deficiency; atherosclerosis; nutritional deficiency; gene therapy; human; ATP-binding cassette; sitosterolaemia susceptibility gene; SSG; 20-NOV-2000; 2000US-252235P. 28-NOV-2000; 2000US-253645P. 20-NOV-2001; 2001WO-US43823 17-OCT-2002. WO200281691-A2 Homo sapiens

Human ABCG5 mutant

Hobbs HH,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New ABCG8 polypeptides and nucleic acids, useful for treating sterol-related disorders e.g. sitosterolemia, hypercholesterolemia, hyperlipidemia, gall stones, HDL deficiency, atherosclerosis, or nutritional deficiencies -
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                                                                                           CCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCF
                                                                                                       CCRIMALAAAALLPTFHMASFESNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCF 600
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ilarity 100.0%;
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RESULT 3
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28-NOV-2000;
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                                                                  (TULA-) TULARIK INC.
(TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                       20-NOV-2001;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New ABCG8 polypeptides and nucleic acids, useful for treating sterol-related disorders e.g. sitosterolemia, hypercholesterolemia, hyperlipidemia, gall stones, HDL deficiency, atherosclerosis, or nutritional deficiencies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22;
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                                                                                                                                                                                                                               ELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVF
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                                                                        SGLMQIQENGHLYTTQIGNETESILGDTMISAMDLNSHPLYAIYLIVIGISYGELFLYYL
                                                                                                                                                                                                                 ELEDGLYTAGPYFFAKILGELPEHCAYVIIYAMPIYWLTNLRPVPELFLLHFLLVWLVVF
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Pred. No. 3.7e-287;
3; Mismatches 68; 1
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The invention relates to human transporters and ion channels (TRICH)

Dolypeptides, a naturally occurring amino acid sequence 90 % identical to TRICH, a biologically active fragment of TRICH or an immunogenic fragment of TRICH. Also included are an isolated polynucleotide encoding TRICH, a recombinant polynucleotide comprising a promoter sequence operably considered to the TRICH polynucleotide, a cell transformed with the crecombinant polynucleotide, an isolated antibody that binds specifically to TRICH, and screening for compounds which bind to TRICH, modulate TRICH expression or are ant/agonists of TRICH.

The polypeptides are useful for diagnosing, treating, and correventing transport, neurological, muscule, immunological disorders (e.g. scleroderma, systemic lupus crythematosus, allergies), cell proliferative disorders such as cancers (e.g. leukaemia, cervical or CC breast cancers), neurological such as cancers (e.g. Parkinson's disease, allergies), neurological musculers (e.g. Parkinson's disease, musculers (e.g. Parkinson's disease, musculers (a.g. Parkinson's disease, musculers (a.g. Parkinson's disease, musculers (e.g. Parkinson's disease).
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03-NOV-2000; 2000US-247673P.
17-NOV-2000; 2000US-247673P.
17-NOV-2000; 2000US-24661P.
20-NOV-2000; 2000US-25233P.
01-DEC-2000; 2000US-250790P.
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Walia NK, rac
Ramkumar J, Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New transporters and ion channels (TRICH) polypeptides, useful diagnosing, preventing, and treating disorders associated with abnormal expression or activity of TRICH, e.g. immunological, more or renal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; transporter and ion channel; TRICH; transport disorder; neurological disorder; muscle disorder; immunological disorder; cance; scleroderma; systemic lupus erythematosus; allergy; leukaemia; cell proliferative disorder; cervical cancer; breast cancer; neurodegenerative disorder; parkinson's disease; Alzheimer's disease; myotonic dystrophy; catatonia; endocrine disorder; diabetes; Grave's disease; gastrointestinal disorder; Crohn's disease; renal disorder; Good pasture's syndrome; viral infection; cirrhosis; bacterial infection; helminthic infection; cardiovascular disorder; protozoal infection; helminthic infection; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 143-144; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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DB; ABK83218.
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, Arvizu C,
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MG, Baughn MR, Gandhi AR, Ding L, Sanjanala M;
rvizu C, Gletzen KJ, Lal PG, Azimzai Y, Khan FA;
Thornton M, Lu DAM, Tribouley CM, Warren BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raumann BE,
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                                             muscular disorders
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Best Local
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Good pasture's syndrome), viral, bacterial, fungal, parasitic, protozoal and helminthic infections, cardiovascular disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis) and many other diseases and disorders detailed in the specification. They can also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels. TRICH or its fragments may also be used in screening for compounds that specifically bind to and modulate the activity of TRICH. The polynucleotides can be used to create knock in humanised animals or transgenic animals to model human disease. The present sequence
                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                          25-FEB-2000;
                                                                                        06-SEP-2000
                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                   17-OCT-2000
                                                                                                                                                                                                                                                                                               AAG18079;
                                                                                                                                                                                                                                                                                                                           AAG18079 standard; Protein;
                                                                                                                                                                             termination
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                                                          2000EP-0301439
99US-0121825.
99US-0123180.
99US-0123548.
                                                                                                                                                                                                                                    protein fragment SEQ ID NO: 19344.
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99.7%;
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Pred. No. 3e-192;
0; Mismatches
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promoter;
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1-OCT-1999
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   537 LYVECCRIMALAAAALLETEHMASEESNALYNSEYLAGGEMINLSSLWTVP---AWISKV 593
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                                                                                                                                                                             MLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVW 536
                                                                                           LLIHGAEACLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSERA 476
                                                                                                                                                                                                                                IKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDK 186
                                                                                                                               --STK-LKAELCNAESHSYEYTKAAAKNLKSEQWCTTWWYQFTVLLQRGVRERRFESFNK 388
                                                                                                                                                       KAETKOLDEDTCVESS----VTPLDTNCLPSPTKMPGAVQQFTTLIRRQI-SNDFRDLPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         QGLPDMSDTQSKSVLAFPTITSQPGLQMSMY-----PITLKFEEVVYKVKI-----E
                           MLIKERSSGMYRLSSYFMARNVGDLPLELALPTAFVFIIYWMGGLKPDPTTFILSLLVVL
                                                                              LRIF---QVISVAFLGGLLWWH-TPKSHIQDRTALLFFFSVFWGFYPLYNAVFTFPQEKR 444
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99US-0161405.
99US-0161406.
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990S-0162142
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990S-0161360
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99US-0158232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 730.5; DB 21;
Pred. No. 2e-65;
17; Mismatches 269;
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25-MAY-1999;
27-MAY-1999;
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01-JUN-1999;
                                                                                                    20-MAY-1999
21-MAY-1999
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                                                                                                                                                                                                                                                                      04-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2000
                                                                                                                               19-MAY-1999;
                                                                                                                                           18-MAY-1999
                                                                                                                                                                                 14-MAY-1999
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29-MAR-1999
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09-MAR-1999;
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                                                               99US-0135629.
99US-0136021.
99US-0136392.
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99US-0134219.
99US-0134221.
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99US-0132048.
99US-0132407.
990S-0137528
990S-0137502
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8-JUN-1999; 0-JUN-1999; 0-JUN-1999;

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1-1999 1-1999; 1-1999;

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Query Match 20.8%; Score 730.5; DB 21. Best Local Similarity 30.7%; Pred. No. 2.1e-65; Matches 211; Conservative 117; Mismatches 269;
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13-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
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13-SEP-1999;
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31-AUG
01-SEP
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Indels Length 648;

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990S-0139750
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      25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 19345.
                                                                                                                                                                                                                                                                                                                          AAG18080 standard; Protein; 625 AA.
                                                                                 06-SEP-2000
                                                                                                               EP1033405-A2
                                                                                                                                         Arabidopsis thaliana.
                                               25-FEB-2000; 2000EP-0301439
                                                                                                                                                                         termination
                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 KAETKDLDEDTCVESS----VTPLDTNCLPSPTKMPGAVQQFTTLIRRQI-SNDFRDLPT
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TAHRIVTTIKRLASGGRTVVTTIHQPSSRIYHMFDKVVLLSEGSPIYYGAASSAVEYFSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFLRWCFEGLMKIQFSRRTY-------KMPLGNLTIAVSGDKILSAMEL
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                                                                                                                                                                       sequence.
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                                                                                                                                                                                    promoter;
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99US-0142154.

99US-0142355.

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99US-0143542.

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990S-0154758

990S-0154018

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07-0CT-1999
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SSGMYRLSSYFMARNVGDLPLELALPTAFVFIIYWMGGLKPDPTTFILSLLVVLYSVLVA
          EDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCC
                                  MYNGQPFSGCIKRR-TGFVAQDDVLYPHLTVWETLFFTALLRLPSSLTRDEKAEHVDRVI
                                                                                                                                                                                                                                    WINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVI
                                                                                                                                                                                                                                                             MPWTSPSCONSCELGIONLSFKVRSGOMLAIIGSSGCGRASLLDVTTGRGHGGKIKSGQI
                                                                      LKAELCNAESHSYEYTKAAAKNLKSEQWCTTWWYQFTVLLQRGVRERRFESFNKLRIF--
                                                                                         LDEDTCVESS----VTPLDTNCLPSPTKMPGAVQQFTTLIRRQI-SNDFRDLPTLLIHGA 422
                                                                                                                                                                                                                                                                                                                                       20.7%; Score 724; DB 21; illarity 30.9%; Pred. No. 9.3e-65; Conservative 113; Mismatches 258;
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990S-0158239
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990S-0161359
990S-0161359
990S-0161359
990S-0161392
                                                                                                                                                                                                                                                                                                                                                  20.7%;
                                                                                                                                                                                                                                                                                                                                                         Length 625;
                                                                                                                                                                                                                                                                                                                                       Indels 100;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                    312
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                                                                                                                                                                                                                                             192
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10-AUG-1999

-1999

-AUG-1999

18-AUG
20-AUG
20-AUG
20-AUG
20-AUG
23-AUG
23-AUG
25-AUG
27-AUG
27

1999 1999;

-AUG-1999; 5-AUG-1999; 5-AUG-1999; -AUG-1999;

-1999 -1999 -1999

;-1999; ;-1999;

-SEP-1999;

-1999; -1999; -1999; -1999;

-1999

1999

-1999; -1999;

02-AUG-1999 03-AUG-1999 04-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 09-AUG-1999

-JUL-1999;

-JUL-1999

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RESULT 8
AAU96986
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                                                                       culture or mammal which have ABCCS polypeptide with a compound and measuring ABCGS biological activity in the cell culture or in mammal, where an increase or decrease in ABCGS biological activity on a control cell culture or mammal of ABCGS biological activity in a control cell culture or mammal or decreases ABCGS activity respectively. The cell culture or mammal comprises a mutated ABCGS polypeptide or a wild type polypeptide. The ABCGS biological activity, or level of ABCGS mRNA, or level of the polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal comprising a wild type ABCGS polypeptide. Stimulation of ABCGS activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's
                                                                                                                                                                                                                                                                                       The present invention relates to a new mammalian ATP-binding cassett gene 5 (ABCG5) polypeptide. The invention is useful for identifying predisposition for developing sitosteroclemia, arteriosclerosis or he disease. The molecules of the invention are also useful for identify a compound which alters ABCG5 activity level comprising contacting a
                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel mammalian ATP-binding cassette gene 5 polypeptide, a nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-416483/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patel SB, Dean M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat ABCG5 protein
                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 45; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B. (DEAN/) DEAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2001; 2001WO-US29859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200227016-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-2000; 2000US-235268P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK51686.
                                      rolemia, arteriosclerosis, heart quisease under method of the invention is useful for in the method of the invention adsorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A----YMALHRVKLR 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEGLMKIQFSRRTY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGLGLAFGALLMNIKQATTLASVTTLVFLIAGGYYVQ-----QIPPFIVWLKYLSYSYYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVP---AWISKVSFLRWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                           for increasing cholesterol tion. The present amino
                                                                                                                                                                                                                                                                                                             for identifying
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KW Huma

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Best Local Similarity
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                                                                                                                                                                                                                                                                                         Human; ABCG5; ATP-binding cassette gene 5; sitosterólemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
                            WO200227016-A2
                                                                                                            Misc-difference
                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                        mutant;
                                                                                                                                                                                                                                                                                                                                                                           Human ABCG5 mutant R389H protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU96990 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386 VVIMRLVQNLIMGLFLIFYLLRVQNNMLKGAVQDRVGLLYQLVGATPYTGMLNAVNLFPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERAMLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPCPRYSNPADFYVDLTSIDRRSREQELATREKAQSLAALF-----LEKVRDL 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGEVFVNGCELRRDQFQDCVSYLLQSDVFLSSLTVRETLRYTAMLAL-RSSSADFYDKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEGARGPHNNRGSQ----SSLEEGSV--TGSEARHSLGV--LNVSFSVSNRVGPW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KTLPM----VPFKTKNPPGMFCKLGVLLRRVTRNLMRNKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPCPEHSNPFDFYMDLTSVDTQSREREIETYKRVQMLESAFRQSDICHKILENIERTRHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAVLTELSLSHVADQMIGNYNFGGISSGERRRVSIAAQLLQDPKVMMLDEPTTGLDCMTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----WNIKSCQQKWDRKILKDVSLYIESGQTMCILGSSGSGKTTLLDAISGRLRRTGTL 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                      Location/Qualifiers 389
                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                                                                         "Wild-type Arg
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Pred. No. 1.3e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new mammalian Amp-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to never historical activity in the cell culture or in mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: This sequence is not shown in the specification but is derived from the wild-type human ABCG5 protein (AAU96984) given on pages 35-of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel mammalian ATP-binding cassette gene 5 polypeptide, nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
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SNPADFYVDLTSIDRRSREQELATREKAQSLAALF-
                                                       LVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEH
                                                                             LSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHWQQYFTAIGYPCPRY
                                                                                                                               LSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVL
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The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal,

Claim 52;

Page 35-36; 66pp;

English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          decreases ABCG5 activity respectively. The cell culture or mammal comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The ABCG5 biological activity, or level of ABCG5 mRNA, or level of the polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal swild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's
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(first entry)
                                                                                                                                                                                                                  -GYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFL
                                                                                                                                                                                                                                                                                                                                                                                                                       -----KTLPM-----VPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.9%; Score 697; DB 28.9%; Pred. No. 5.9e tive 124; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 697; DB 23;
NO. 5.9e-62;
ismatches 241;
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WPI;
                                   Patel SB,
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Misc-difference 419
                                                                                           (USSH ) US DEPT HEALTH & HUMAN (PATE/) PATEL S B.
                                                                                                                                                 25-SEP-2000; 2000US-235268P.
                                                                                                                                                                                       25-SEP-2001; 2001WO-US29859
                                                                                                                                                                                                                               04-APR-2002
                                                                                                                                                                                                                                                                     WO200227016-A2
                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                           mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ABCG5; ATP-binding casseti arteriosclerosis; heart disease;
                                                                           (DEAN/) DEAN M.
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ABCG5 mutant R419P protein sequence
                                   Dean M;
                                                                                                                                                                                                                                                                                                     /note= "Wild-type Arg substituted by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cassette gene 5; sitosterolemia; ch
isease; hypersterolemia; Alzheimer's
                                                                                                             SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cholesterol;
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sitosterolemia, arteriosclerosis Novel mammalian ATP-binding cassette gene 5 polypeptide, nucleic acid encoding the polypeptide, useful for treat! Claim 10; Page -; 66pp; English. and heart diseases treating and

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disease. The molecules of the invention are also useful for identifying care compound which alters ABCG5 polypeptide with a compound and coulture or mammal which have ABCG5 polypeptide with a compound and control cell culture or mammal not contacted with the compound, identifies a compound that increases or contacted with the compound, identifies a compound that increases or compound and compound and compound that increases or compound and compound and compound that increases or compound with the compound, identifies a compound that increases or compound with the compound and compound that increases or compound with the compound and compound that increases or compound and compound is also compound with that of a second cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound is also compared with that of a compound is also compound with the compound is also compound with the compound in the cell culture or mammal compound is also compound with the compound is also compound in the cell culture or mammal compound is also compound with the compound is also compound in the compound is also compound in the cell culture or mammal is also compound in the cell culture or mammal is also compound in the cel The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing situsterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying Note: This sequence is not shown in the specification but is derived from the wild type human ABCG5 protein (AAU96984) given on pages 35invention specification. for identifying pages 35-36

Sequence 651 AA;

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Query Match
Best Local
                                                          Matches
                                                        187;
                             16
     œ
                                                                   Similarity
                       TPQDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLASQVPWFEQLAQFKMPW
 TPGGSMGLQVNRGSQSSLEGAPAT-APEPHSLGILHASYSVSHRVR-PWWD-ITSCRQQW
                                                       Conservative
                                                                   19.9%;
28.9%;
                                                       124;
                                                    Score 697; DB 23;
Pred. No. 5.9e-62;
24; Mismatches 241;
                                                                             Length 651;
                                                      Indels
                                                    96;
                                                    Gaps
64
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Ş 76 TSPSCQNSCELGIQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGR-GHGGKIKSGQIWI 134

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RESULT 12
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          Novel sitosterolemia
                                     N-PSDB;
                                                  WPI; 2002-017598/02
                                                                                                                                                                                                                                                                                Human; sitosterolaemia susceptibility gene; SSG; atherosclerosis; sterol-related disorder; hyperlipidaemia; hypercholesterolaemia; tgall stone; coronary heart disease; cardiovascular disease; arthranthoma; haemolytic anaemia; transgenic animal; chromosome 2p21.
                                                                                                                                                                                                                                                                                                                                                       Human sitosterolaemia
                                                                                                                                18-APR-2000; 2000US-198465P.
15-MAY-2000; 2000US-204234P.
                                                                                                                                                                        18-APR-2001; 2001WO-US12758
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                                                                                                        TULARIK INC
                                                                             Schultz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INLSSLWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQNLIMGLFLLFFVLRVRSNVLKGAIQ----DPVGLLYQFVGATPYTGMLNAVNLFPVLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AETKDLDEDTCVESSVTPLDTNCLPSPTK-MPGAVQQFTTLIRRQISNDFRDLPTLLIHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRLRQCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEH
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        susceptibility
                                                                                                                                                                                                                                                                                                                                                 susceptibility gene (SSG) protein
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       gene polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19;
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RNIQEMPIPEKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTN
                                                                                                                                                                                                                                                                                                     SNPADFYVDLTSIDRRSREQELATREKAQSLAALF------LEKVRDLDDFLWK
                                                                                                                                                                                                                                                                                                                               LVELARRNRIVVLTIHOPRSELFOLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEH
                                                                                                                                                                                                                                                                                                                                                 LSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRY
                           INLSSLWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVS
                                                                                                                                     AMLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLV 535
                                                                                                                                                                                            AEACLMSMTIGFLYFG-----HGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSER
                                                                                                                                                                                                                                                                                                                                                                                                      LRLRQCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKT
                                                   -----GYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFL
                                                                                   WLVVFCCRIMALAAAALLPTFHMASFFS---
                                                                                                           AVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARF-----
                                                                                                                                                                 LQNLIMGLFLLFFVLRVRSNVLKGAIQ----DRVGLLYQFVGATPYTGMLNAVNLFPVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                            NGRALRREOFODCFSYVLOSDTLLSSLTVRETLHYTALLAI-RRGNPGSFQKKVEAVMAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 AA;
                                                                                                                                                                                                                     ----KTLPM-----VPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTF-LGEVYV
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115

64 75

--NALYNSFYLAG----GFM 577

499

549

475

421 348 362 294 314 234 254

446

625

polynucleotide, useful for screening a compound that increases the level of expression or activity of SSG polypeptide for treating

(SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP)
CC binding cassette (ABC) family cholesterol transporter. SSG is useful
CC for identifying a compound useful in the treatment or prevention of a
CC sterol-related disorder, including sitosterolaemia, hyperlipidaemia,
CC hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or
CC nutritional deficiencies. SSG is also useful for treating cholesterolCC associated diseases or conditions including ocronary heart disease and
CC including arthritis, xanthomas and chronic haemolytic anaemia. SSG
CC expression cassette is useful in the production of transgenic non-human
CC animals. SSG genes and their homologues are useful as tools for a number
CC cardiovascular disorders, for forensics and paternity determinations,
CC and for treating any of a large number of SSG associated diseases. The
CC present sequence is human SSG protein. Human SSG is located on chromosome to an isolated Sitosterolaemia Susceptibility Gene is located on chromosome

Length Indels 651; 96; Gaps

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Best Local S
Matches 187
                                                                                                                                                                                                                                                                                    transporter, ABCG8 polypeptides and polynucleotides. The invention also provides ABCG5 polypeptides and polynucleotides. ABCG5 gene is also known as sitosterolaemia susceptibility gene (SSG). Sequences of the invention are useful for treating or preventing sterol-related disorders
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                     They are also useful
                                                                                                                                                                                                                                                                 stones, HDL deficiency,
                                                                                                                                                                                                                                                                                                                                   The invention relates to ATP-binding cassette (ABC) family cholestero
                                                                                                                                                                                                                                                                                                                                                              Claim 28; Page 78-79;
                                                                                                                                                                                                                                                                                                                                                                                       nutritional deficiencies
                                                                                                                                                                                                                                                                                                                                                                                            New ABCG8 polypeptides and nucleic acids, useful for treating sterol-related disorders e.g. sitosterolemia, hypercholesterolemia, hyperlipidemia, gall stones, HDL deficiency, atherosclerosis, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2000;
28-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABC family cholesterol transporter; ABCG8; sterol-related disorder; sitosterolaemia; hyperlipidaemia; hypercholesterolaemia; gall stone; HDL deficiency; atherosclerosis; nutritional deficiency; gene therapy; human; ATP-binding cassette; sitosterolaemia susceptibility gene; SSG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ABCG5
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                                                                                                                                                                               Similarity
                                                                  NGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAE
LRLRQCADTRYGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKT 254
                                                                                                                                         TPQDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLASQVPWFEQLAQFKMPW
                      NGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAI-RRGNPGSFQKKVEAVMAE
                                                                                                                    TPGGSMGLQVNRGSQSSLEGAPAT-APEPHSLGILHASYSVSHRVR-PWWD-ITSCRQQW
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              Novel mammalian ATP-binding cassette gene nucleic acid encoding the polypeptide, use sitosterolemia, arteriosclerosis and heart
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                                                                                                                                                                                     Patel SB, Dean M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ABCG5 mutant R419H protein sequence
                                                                                                                                                                                                                                                                                                                                                              25-SEP-2000; 2000US-235268P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAE
                                                                                                                                                                              LQNLIMGLELLEFVLRVRSNVLKGAIQ-----DHVGLLYQFVGATPYTGMLNAVNLFPVLR
                                                                                                                                                                                                                          AEACLMSMTIGFLYFG-----HGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSRLARGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRLRQCADTRYGNMYVRGLSGGERRRYSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKT
                                               WLVVFCCRIMALAAALLPTFHMASFES-----
                                                                                       AVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARF------
                                                                                                                               AMLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLV
                                                                                                                                                                                                                                                                                                               AETKDLDEDTCVESSVTPLDTNCLPSPTK-MPGAVQQFTTL1RRQ1SNDFRDLPTLL1HG
                                                                                                                                                                                                                                                                                                                                                         SNPADFYVDLTSIDRRSREQELATREKAQSLAALF-----LEKVRDLDDFLWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSLSHVADRLIGNYSLGGISTGERRRYSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAI-RRGNPGSFQKKVEAVMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRQI-----LKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTF-LGEVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPGGSMGLQVNRGSQSSLEGAPAT-APEPHSLGILHASYSVSHRVR-PWWD-ITSCRQQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPQDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLASQVPWFEQLAQFKMPW
                                                                                                                                                                                                                                                                     -----KTLPM----VPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a new mammalian ATP-binding cassette
-GYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 696; DB 23;
Pred. No. 7.5e-62;
24; Mismatches 241;
                                          ----NALYNSFYLAG-----GFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 651;
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RESULT 15
AAU96992
AU AAU96
XX AAU96
XX AAU96
XX Human
XX Human
XX Human
XX Human
XX Human
XX Homo
OS Synth
XX WO200
PM WO200
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XX Homo
OS Synth
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XX Homo
OS Synth
XX WO210
PM WO200
XX Homo
OS Synth
XX WO210
PM WO200
XX Homo
OX 
                                                                                                                                           The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABGG5) polypeptide. The invention is useful for identifying a credisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying a compound which alters ABGG5 activity level comprising contacting a cell culture or mammal which have ABGG5 polypeptide with a compound and comeasuring ABGG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABGG5 biological activity compared to contacted with the compound, identifies a compound that increases or contacted with the compound, identifies a compound that increases or contacted with the compound, identifies a compound that increases or contacted with the compound, identifies a compound that increases or contacted with the compound, identifies a compound that increases or comparises a mutated ABGG5 polypeptide or a wild type polypeptide. The CC polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is useful for treating or preventing configuration and/or ABGG5 activity is useful for increasing cholesterol acid sequence represents the human ABGG5 mutant E146Q protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ф
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(PATE/) PATEL S 1
(DEAN/) DEAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page -; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel mammalian ATP-binding cassette gene 5 polypeptide, a nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-416483/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200227016-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550 RNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTN 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INLSSLWTVPAWISKYSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Note: This sequence is no from the wild-type human

is not shown in the specification but is numan ABCG5 protein (AAU96984) given on pa

; derived bages 35-36

Оy	B	Qy	Ф	Oy	Db	Qy	DЬ	Qy	DЬ	Qy	Db	Qy	Db	Qy	Db	γo	οъ	Qy	DЬ	Qy	Query M Best Lo Matches	so s
578 : 550 1	500	536 1	447	476	391	422	349	363	295	315	235	255	175	195	116	135	65	76	80	16	/ Match Local nes 18	Sequence
INLSSLWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVS 625 	GYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFL 549	WLVVFCCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGEM 577	AVSDQESQDGLYQKWQMMLAYALHVLPFSVVATNIFSSVCYWTLGLHPEVARF 499	AMLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLV 535	QNLIMGLELLEFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFDVLR 446	AEACLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSER 475	KTLPMVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRL 390	AETKDLDEDTCVESSVTPLDTNCLPSPTK-MPGAVQQFTTLIRRQISNDFRDLPTLLIHG 421	SNPFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHL 348	SNPADFYVDLTSIDRRSREQELATREKAQSLAALFLEKVRDLDDELWK 362	LVELARRNRIVVLTIHOPRSELFOLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEH 294	₹	LSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDFKVMLFDEPTTGLDCMTANQIVVL 234	LRLRQCADTRVGNMYVRGLSGGERRRVSIGVQLLMNPGILILDEPTSGLDSFTAHNLVKT 254	NGRALRREQFQDCFSYVLQSDTLLSSLTVRQTLHYTALLAI-RRGNPGSFQKKVEAVMAE 174	NGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAE 194	TRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTF-LGEVYV 115	TSPSCQNSCELGIQNLSFKVRSGQMLAIIGSSGCGRASLLDVITGR-GHGGKIKSGQIWI 134	TPGGSMGLQVNRGSQSSLEGAPAT APEPHSLGILHASYSVSHRVR-PWWD-ITSCRQQW 64	TPQDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLASQVPWFEQLAQFKMPW 75	19.8%; Score 694; DB 23; Length 651; Similarity 28.7%; Pred. No. 1.2e-61; 6; Conservative 125; Mismatches 241; Indels 96; Gaps 16;	651 AA;

Search completed: July 25, 2003, 17:12:13 Job time: 90 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                              Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the
                                                                                                                                            Score
                                                                                                                                                                                                                               is the number of results predicted by ater than or equal to the score of the
                                         100.0
63.0
56.2
53.6
10.9
7.6
                                                                                                                                              Match
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2669
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
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AAD48882
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11156.341 Million cell updates/sec
                                                                                                                                                                                                                            result being printed,
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   Mouse ABCG8 DNA.

Arabidopsis EST-de
DNA encoding human
Human sitosterolae
Human ABCG5 DNA.
                                                                                                                                       Description
                                                                                              Human
                                                                                                          Human ABCG8 DNA.
                                                                              Mouse clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . DAT: *
                                                                          transporter
clone IMX3_6
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AAD48883
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20-NOV-2000; 2000US-252235P.
28-NOV-2000; 2000US-253645P.
                                         20-NOV-2001; 2001WO-US43823
                                                                          17-OCT-2002.
                                                                                                       WO200281691-A2.
                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                 Human ABCG8 DNA.
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ALIGNMENTS

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DT 24-MAR-2003 (first entry)

XX

DE Human ABCG8 DNA.

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XX

ABC family cholesterol transporter; ABCG8; sterol-related disorder; kW sitosterolaemia; hyperlipidaemia; hypercholesterolaemia; gall stone; kW HDL deficiency; atherosclerosis; nutritional deficiency; gene therapy; kW human; ATP-bliding cassette; sitosterolaemia susceptibility gene; SSG; XX

KW ABCG5; gene; ds.

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Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transporter, ABCGS polypeptides and polynucleotides. The invention also provides ABCGS polypeptides and polynucleotides. ABCGS gene is also known as sitosterolaemia susceptibility gene (SSG). Sequences of the invention are useful for treating or preventing sterol-related disorders such as sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis and nutritional deficiencies. They are also useful in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New ABCG8 polypeptides and nucleic acids, useful for treating sterol-related disorders e.g. sitosterolemia, hypercholesterolemia, hyperlipidemia, gall stones, HDL deficiency, atherosclerosis, or nutritional deficiencies
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Human transporter and ion channel, TRICH9,
gene;
                               Incyte ID
                              6585710CB1, cDNA.
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27-AUG-2002

entry;

cell proliferative disorder; cervical cancer; breast cancer; neurodegenerative disorder; Parkinson's disease; Alzheimer's diseas myotonic dystrophy; catatonia; endocrine disorder; diabetes; Grave's disease; gastrointestinal disorder; Crohn's disease; renal disorder; Good pasture's syndrome; viral infection; cirrhosis bacterial infection; fungal infection; parasitic infection; protozoal infection; helminthic infection; cardiovascular disorder; atherosclerosis; scleroderma; systemic lupus erythematosus; allergy; leukaemia; ene; transporter and ion channel; TRICH; transport disorder; disorder; muscle disorder; immunological disorder; cancer; hepatic disease cirrhosis; disease;

Homo sapiens.

WO200240541-A2

23-MAY-2002

25-OCT-2001; 2001WO-US46055

27-OCT-2000; 03-NOV-2000; 09-NOV-2000; 17-NOV-2000; 20-NOV-2000; ; 2000US-243989P. ; 2000US-247673P. ; 2000US-247673P. ; 2000US-249661P. ; 2000US-252232P. ; 2000US-250790P.

(INCY-) INCYTE GENOMICS INC

Walia NK, Thangavelu Ramkumar , c d, Das D, Yue H, Yao MG, ne H, Nguyen DB, Hafalia AJA, Elliott VS, Lu Y; Aao MG, Baughn MR, Gandhi AR, Ding L, Sanjanwala M; Arvizu C, Gietzen KJ, Lal PG, Azimzai Y, Khan FA; Thornton M, Lu DAM, Tribouley CM, Warren BA; IS D, Raumann BE, Policky JL, Kearney L;

2002-463570/49 DB; ABG61539.

P-PSDB;

New transporters and ion channels (TRICH) polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of TRICH, e.g. immunological, muscular or renal disorders

Claim 5; Page 167-168; 178pp; English

The invention relates to human transporters and ion channels (TRICH)
CC polypeptides, a naturally occurring amino acid sequence 90 % identical to
CC TRICH, a biologically active fragment of TRICH or an immunogenic fragment
CC of TRICH. Also included are an isolated polynucleotide encoding TRICH,
CC a recombinant polynucleotide, a cell transformed with the
CC recombinant polynucleotide, a transgenic organism comprising the
CC recombinant polynucleotide, an isolated antibody that binds specifically
CC to TRICH, modulate TRICH expression or are ant/agonists of TRICH, modulate TRICH expression or are ant/agonists of TRICH.
CC The polypeptides are useful for diagnosing, treating, and
CC preventing transport, neurological, muscle, immunological disorders
CC (e.g. scleroderma, systemic lupus erythematosus, allergies), cell
CC proliferative disorders such as cancers (e.g. leukaemia, cervical or
CC proliferative disorders such as cancers (e.g. Parkinson's disease,
CC Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,
CC gastrointestinal disorders (e.g. Crohn's disease), renal disorders
CC (e.g. Good pasture's syndrome), viral, bacterial, fungal, parasitic,
CC extensions, or hepatic diseases (e.g. cirrhosis) and many
CC other diseases and disorders detailed in the specification. They can also
CC be used in assessing the effects of exogenous compounds on the
CC expression of nucleic acid and amino acid sequences of transporters and

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ABN90022 standard;

16-AUG-2002

Mouse clone IMX3_67 extended sequence.

Mouse; a digital antiinflammatory; sequence tag; total gene expression gene therapy; ileitis; DST;

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Best Local :
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ABC family cholesterol transporter; ABCG8; sterol-related disorder; sitosterolaemia; hyperlipidaemia; hypercholesterolaemia; gall stone; HDL deficiency; atheroscierosis; nutritional deficiency; gene therapy; mouse; ATP-binding cassette; sitosterolaemia susceptibility gene; SSG; ABCG5; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New ABCG8 polypeptides and nucleic acids, useful for treating
sterol-related disorders e.g. sitosterolemia, hypercholesterolemia,
hyperlipidemia, gall stones, HDL deficiency, atherosclerosis, or
nutritional deficiencies
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03-AUG-2000;
15-SEP-2000;
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                                                                                                                                                                    DNA encoding
         WO200227016-A2
                                                                                                                           chromosome 2p21;
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                                                                                                                                                                                                                                  ABK51681 standard; DNA; 1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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P-PSDB; AAM24252.
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                                                                                                                                                                    human ABCG5 protein.
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                         /product= "Human ABCG5 protein"
/transl_except= (pos: 4..9, aa:
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from expressed sequence tags (ESTs)
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cc predisposition for developing sitosterolemia, arteriosclerosis or heart C disease. The molecules of the invention are also useful for identifying ca compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and cell culture or mammal which have ABCG5 polypeptide with a compound and comeasuring ABCG5 biological activity in the cell culture or in mammal. C where an increase or decrease in ABCG5 biological activity compared to C ABCG5 biological activity in a control cell culture or mammal not c contacted with the compound, identifies a compound that increases or C decreases ABCG5 activity respectively. The cell culture or mammal c comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The C ABCG5 biological activity, or level of ABCG5 mRNA, or level of the C colliurity or level of ABCG5 mRNA, or level of the C colliurity or mammal is also compared with that of a second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal is also compared with that of a c second cell culture or mammal compared with that of a c second cell culture or mammal or mammal or mammal compared with that of a c second cell culture or mammal compared with that of a 
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new mammalian ATP-binding gene 5 (ABCG5) polypeptide. The invention is useful for iden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 38; Page 36-37; 66pp; English.
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1920 BP; 440 A; 503 C; 486 G; 491 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dean M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide. The invention is useful for identifying
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7.6%;

Score 203.6; DB 2 Pred. No. 3.4e-44;

DB 24;

Length

Query Match Best Local Similarity Matches 432; Conserv 383 575 323 515 263 455 203 395 143 335 ATCCCGGCTCCTTCC--TCTCCCAGGCCCAGCGTGACAAAAGGGTGGAGGACGTGATCGCGGAGCTGCGGCTTAGGC 694 CCAACTTGACTGTGCGAGAGACCTTGGCCTTCATTGCCCAGATGCGGGCTGCCCAGAACCT 634 TGCGCCGGGAGCAGTTCCAGGACTGCTTCTCCTACGTCCTGCAGAGCGACACCCTGCTGA CCGGCAGGCTGGGGGCGCGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGCGC CTGGCCGAGGTCACGGCGGCAAGATCAAGTCAGGCCAGATCTGGATCAATGGGCAGCCCA 514 AGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGACGCCATGT AGATGCTGGCCATCATAGGGAGCTCAGGTTGTGGGAGAGCCTCCTTGCTAGATGTGATCA 454 GCTCGCCTCAGCTGGTGAGGAAGTGTGTGGCCCACGTGCGCCAGCACAACCAGCTGCTCC 574 GCCGGCAGCAGTGGACCAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGC GCTGCCAGAATTCTTGTGAGCTGGGCATCCAGAACCTAAGCTTCAAAGTGAGAAGTGGGC GCAGCCTCACCGTGCGCGAGACGCTGCACTACACCGCGCTGCTGGCCATCCGCCGCGCGCA Conservative 0; Mismatches 359; ų. Gaps 442 499 382 322 202 394 262

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Novel sitosterolemia susceptibility gene polypeptide and polynucleotide, useful for screening a compound that increases the
                                                      WPI; 2002-017598/02
P-PSDB; AAE13290.
                                                                                                  Tian H,
                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                               Human; sitosterolaemia susceptibility gene; SSG; atherosclerosis; sterol-related disorder; hyperlipidaemia; hypercholesterolaemia; thera gall stone; coronary heart disease; cardiovascular disease; arthritis; xanthoma; haemolytic anaemia; transgenic animal; chromosome 2p21; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD22009
                                                                                                                                                              18-APR-2000;
15-MAY-2000;
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                                                                                                                                                                                                              18-APR-2001; 2001WO-US12758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human sitosterolaemia susceptibility gene (SSG).
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2000US-204234P.
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Best Local S
Matches 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated Sitosterolaemia Susceptibility Gene (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) binding cassette (ABC) family cholesterol transporter. SSG is useful for identifying a compound useful in the treatment or prevention of a sterol-related disorder, including sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or nutritional deficiencies. SSG is also useful for treating cholesterol-associated diseases or conditions including coronary heart disease and other cardiovascular diseases, and sitosterolaemia-associated condition including arthritis, xanthomas and chronic haemolytic anaemia. SSG expression cassette is useful in the production of transgenic non-human animals. SSG genes and their homologues are useful as tools for a number of annitarions including disconsions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of applications including diagnosing sitosterolaemia and other cardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The present sequence is human SSG DNA. Human SSG is located on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sterol-related
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                             TGTTTGATCTGGTCCTGCTGATGACGTCTGGCACCCCCATCTACGTGGGGGGGCCCAGC
                                                                                                                                                             CCACCTCTGGGCTCGACAGCTTCACAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGG
                                                                                                                                                                                                                      GGAGAGTCAGCATTGGGGTGCAGCTCCTGTGGAACCCAGGAATCCTTATTCTCGACGAAC
                                                                                                                                                                                                                                                                                                                             ATCCCGGCTCCTTCC---AGAAGAAGGTGGAGGCCGTCATGGCAGAGCTGAGTCTGAGCC
                                                                                                   CCAAAGGCAACCGGCTGGTGCTCATCTCCCTCCACCAGCCTCGCTCTGACATCTTCAGGC
                                                                                                                                    CAACCACAGGCCTGGACTGCATGACTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTGG
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           TCTTTGACAAAATTGCCATCCTGAGCTTCGGAGAGCTGATTTTCTGTGGCACGCCAGCGG
                                                                         CTCGCAGGAACCGAATTGTGGTTCTCACCATTCACCAGCCCCGTTCTGAGCTTTTTCAGC
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Pred. No. 3.1
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Indels Length

Gaps

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                                                             The invention relates to ATP-binding cassette (ABC) family cholesterol transporter, ABCGB polypeptides and polynucleotides. The invention also provides ABCG5 polypeptides and polynucleotides. ABCG5 gene is also known as sitosterolaemia susceptibility gene (SSG). Sequences of the invention are useful for treating or preventing sterol-related disorders such as sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atheroscierosis and nutritional deficiencies. They are also useful in gene therapy. The present sequence is human again.
                                                                                                                                                                                                                                                                                                                                                                                 New ABCG8 polypeptides and nucleic acids, useful for treating
sterol-related disorders e.g. sitosterolemia, hypercholesterolemia,
hyperlipidemia, gall stones, HDL deficiency, atherosclerosis, or
nutritional deficiencies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABC family cholesterol transporter; ABCG8; sterol-related disorder; sitosterolaemia; hyperlipidaemia; hypercholesterolaemia; gall stone; HDL deficiency; atherosclerosis; nutritional deficiency; gene therapy; human; ATP-binding cassette; sitosterolaemia susceptibility gene; SSG;
                                                                                                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-058548/05.
P-PSDB; AAE31704.
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28-NOV-2000; 2000US-253645P
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                                                                                                                                                                                                                                                                                                                                     Page 77;
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Query Match

Sequence 2340

BP;

541 A; 601

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598 G;

600 T; 0 other; B 25;

Score 203.6;

Length 2340;

arteriosclerosis; heart disease; hypersterolemia;

Alzheimer'

cholesterol; r's disease;

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ABK51682
ID ABK5
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                                                 Human; ABCG5; ATP-binding cassette gene 5; sitosterolemia;
                                                                                                                             Human
                                                                                                                                                                                     30-JUL-2002
                                                                                                                                                                                                                                                    ABK51682;
                                                                                                                                                                                                                                                                                                                   ABK51682 standard;
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Best Local Similarity 54.4
Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or manmal not contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or manmal comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The ABCG5 biological activity, or level of ABCG5 mRNA, or level of the polypeptide in a cell culture or manmal is also compared with that of a second cell culture or manmal is also compared with that of a stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 37-38; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid encoding the polypeptide, useful for t
sitosterolemia, arteriosclerosis and heart diseases
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                              CCAACTTGACTGTGCGAGAGACCTTGGCCTTCATTGCCCAGATGCGGCTGCCCAGAACCT 634
                                                                     TGCGCCGGGAGCAGTTCCAGGACTGCTTCTCCTACGTCCTGCAGAGCGACACCCTGCTGA
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                                                                                                                                                                                                                   AGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGACGCCATGT 438
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Pred. No. 3.9e-44;
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                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B. (DEAN/) DEAN M.
                                                                                                           25-SEP-2001; 2001WO-US29859
                                                                                                                                       04-APR-2002
                                                                                                                                                             WO200227016-A2.
                                                                                                                                                                                                                                                                         Rat; ABCG5; ATP-binding cassette gene 5; sitosterolemia; arteriosclerosis; heart disease; hypersterolemia; Alzheim
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                                                                                                                                                                                                                                                                                                                                                                     ABK51686;
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                                                                                    25-SEP-2000; 2000US-235268P
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WPI; 2002-416483/44 P-PSDB; AAU96986.

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                                                                                                                                                                                                                                                                                                       25-SEP-2001; 2001WO-US29859
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/transl_except= (pos: 1912..1915, aa: LGIVIFKVRDYLISR)
/note= "This sequence lacks a stop codon"
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The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of thorention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or mammal mathematical activity respectively. The cell culture or mammal mathematical culture or mammal culture o

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53.48;
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Pred. No. 1.9e-41;
0; Mismatches 371;
981
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RESULT

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302

CCGGGAGGCTGCGGCGCACTGGGACCCTGGAAGGGGAGGTGTTTGTGAATGGCTGCGAGC CTGGCCGAGGTCACGGCGGCAAGATCAAGTCAGGCCAGATCTGGATCAATGGGCAGCCCA AGATTATGTGCATCTTAGGCAGCTCAGGCTCAGGGAAGACCACGCTGCTGGACGCCATCT

514 301

455 242 395 182

AGATGCTGGCCATCATAGGGAGCTCAGGTTGTGGGAGAGCCTCCTTGCTAGATGTGATCA 454

GCCAGCAGAAGTGGGACAGGCAAATCCTCAAAGATGTCTCCTTGTACATCGAGAGTGGCC GCTGCCAGAATTCTTGTGAGCTGGGCATCCAGAACCTAAGCTTCAAAGTGAGAAGTGGGC

241 394

밁 Q

Query Match Best Local S Matches 429

Similarity

7.28;

Score 193.4; Pred. No. 2e-

2e-41; DB 25; 371;

429;

Conservative

0;

Mismatches

Indels Length

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Gaps

Sequence 1959

BP;

468 A; 506 C; 495 G;

490 T; 0 other;

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ID AAD4
XX
AC AAD4
XX
                                                                                                                      The invention relates to ATP-binding cassette (ABC) family cholesterol transporter, ABCG8 polypeptides and polypucleotides. The invention also provides ABCG5 polypeptides and polypucleotides. ABCG5 gone is also known as sitosterolaemia susceptibility gene (SSG). Sequences of the invention are useful for treating or preventing sterol-related disorders such as sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atheroscierosis and nutritional deficiencies.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New ABCG8 polypeptides and nucleic acids, useful for treating sterol-related disorders e.g. sitosterolemia, hypercholesterolemia, hyperlipidemia, gall stones, HDL deficiency, atherosclerosis, or nutritional deficiencies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABC family cholesterol transporter; ABCG8; sterol-related disorder; sitosterolaemia; hyperlipidaemia; hypercholesterolaemia; gall stone; HDL deficiency; atherosclerosis; nutritional deficiency; gene therapy; mouse; ATP-binding cassette; sitosterolaemia susceptibility gene; SSG; ABCG5; gene; ds.
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28-NOV-2000;
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(TEXA ) UNIV TEXAS SYSTEM
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                                                                                        are also useful in gene therapy. The present sequence
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2000US-253645P
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AC AAD22
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MOUSE
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MOUSE
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KW MOUSE
KW Stero
KW Gall
KW XANTH
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PH Key
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18-APR-2001;
                           25-OCT-2001.
                                                     W0200179272-A2
                                                                                                                                                                      Mouse; sitosterolaemia susceptibility gene; SSG; atherosclerosis; sterol-related disorder; hyperlipidaemia; hypercholesterolaemia; gall stone; coronary heart disease; cardiovascular disease; arthranthoma; haemolytic anaemia; transgenic animal; chromosome 17; d.
                                                                                                                                                   Mus sp
                                                                                                                                                                                                                                           Mouse sitosterolaemia susceptibility gene (SSG).
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                                                                                                                                                                                                                                                                                                                                                                                                                          GGGAGAAGGCTCAGTCACTCGCA 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTTCGACAAAATTGCCATCCTGACTTACGGAGAGTTGGTGTTCTGTGGCACCCCAGAGG
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2001WO-US12758
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                          Location/Qualifiers
                                                                             product- "Mouse SSG
                                                                                                                                                                                                                                                                                                                                 2258
                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                        sease; cardiovascular disease; arthritis; transgenic animal; chromosome 17; ds.
                                                                             protein'
                                                                                                                                                                                                therapy;
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The invention relates to an isolated Sitosterolaemia Susceptibility Gene (C (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) c binding cassette (ABC) femily cholesterol transporter. SSG is useful C for identifying a compound useful in the treatment or prevention of a CC sterol-related disorder, including sitosterolaemia, hyperlipidaemia, c hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or nutritional deficiencies. SSG is also useful for treating cholesterol-c associated diseases or conditions including coronary heart disease and c other cardiovascular diseases, and sitosterolaemia-associated condition including arthritis, xanthomas and chronic haemolytic anaemia. SSG expression cassette is useful in the production of transgenic non-human C animals. SSG genes and their homologues are useful as tools for a number C of applications including diagnosing sitosterolaemia and other cardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The present sequence is mouse SSG DNA. Mouse SSG is located on chromosome 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel sitosterolemia susceptibility gene polypeptide and polynucleotide, useful for screening a compound that increases the level of expression or activity of SSG polypeptide for treating
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 7; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sterol-related disorder
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15-MAY-2000;
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DB; AAE13289.
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2000US-204234P.
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Query Match 2258 BP; 549 A; 579 C; 567 G; 563 T; 0 other; 7.28; 53.48; Score 193.4; DB 24; Pred. No. 2.1e-41; Length

Matches

429;

Conservative

0;

Mismatches

371;

Indels

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Similarity

В Qy B Qy В δÃ 밁 δÃ Вb δÃ 밁 Š В Ş 밁 Š 645 695 525 468 408 395 AGATGCTGGCCATCATAGGGAGGCTCAGGTTGTGGGAGAGGCCTCCTTGCTAGATGTGATCA 454 335 GCTGCCAGAATTCTTGTGAGCTGGGCATCCAGAACCTAAGCTTCAAAGTGAGAAGTGGGC 228 GCCAGCAGAAGTGGGACAGGCAAATCCTCAAAGATGTCTCCTTGTACATCGAGAGTGGCC GCGAGTTTCCATCGCAGCCCAACTCCTTCAGGACCCCAAGGTCATGATGCTAGATGAGC GGAGAGTCAGCATTGGGGTGCAGCTCCTGTGGAACCCAGGAATCCTTATTCTCGACGAAC 814 GCTCCGCGGACTTCTACAACAAGAAGGTAGAGGCAGTCATGACAGAGCTGAGCCTGAGCC TCTCCCAGGCCCAGCGTGACAAAAGGGTGGAGGAGCTGATCGCGGAGCTGCGGCTTAGGC CCAACTTGACTGTGCGAGAGACCTTGGCCTTCATTGCCCAGATGCGGCTGCCCAGAACCT 634 CCGGGAGGCTGCGGCGCACTGGGACCCTGGAAGGGGAGGTGTTTGTGAATGGCTGCGAGC CTGGCCGAGGTCACGGCGGCAAGATCAAGTCAGGCCAGATCTGGATCAATGGGCAGCCCA 514 AGATTATGTGCATCTTAGGCAGCTCAGGCTCAGGGAAGACCACGCTGCTGGACGCCATCT ACGTGGCGGACCAAATGATTGGCAGCTATAATTTTGGGGGAATTTCCAGTGGCGAGCGGC AGTGCGCTGACACCCGCGTGGGCAACATGTACGTGCGGGGGGTTGTCGGGGGGGTGAGCGCA GCAGCCTCACTGTGCGCGAGACGTTGCGATACACAGC---GATGCTGGCCCTCTGCCGCA TGCGCAGGGACCAGTTCCAAGACTGCTTCTCCTACGTCCTGCAGAGCGACGTTTTTCTGA GCTCGCCTCAGCTGGTGAGGAAGTGTGTGGCCCAGCTGCGCCAGCAGCAGCAGCTGCTCCC Gaps 467 574 644 754 524 704 584 694 407 287 394

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The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or
                                                                                                                                                                                                                                  Novel mammalian ATP-binding cassette gene 5 polypeptide, a nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200227016-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arteriosclerosis;
                                                                                                                                                                                                          Example 3;
                                                                                                                                                                                                                                                                                                               WPI; 2002-416483/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse ABCG5 cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK51685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTCTATGTGGACCTGACCAGCATTGACAGGCGCAGCAGCAGGAGCAGGAATTGGCCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATGGTCCAGTATTTCACAGCCATCGGCTACCCCTGTCCTCGCTACAGCAATCCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTTGATCTGGTCCTCCTGATGACGTCTGGCACCCCCATCTACTTAGGGGCGGCCCAGC
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                                                                                                                                                                                                  Page 45; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                  Dean M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-235268P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    decreases ABCG5 activity respectively. The cell culture or mammal comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The ABCG5 biological activity, or level of ABCG5 mRNA, or level of the polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal comprising a wild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present nucleic acid sequence represents the CDNA sequence of the mouse ABCG5 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2354 BP; 573 A; 604 C;
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   ACAAGCGAGTACAGATGCTGGAA
                                                                                    ACTTCTATGTGGACCTGACCAGCATTGACAGGCGCAGCAGCAGGAGGAGGAATTGGCCACCA 1114
                                                                                                                                                                                                                                                                                                                                                                                     CCACCTCTGGGCTCGACAGCTTCACAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGAGTCAGCATTGGGGTGCAGCTCCTGTGGAACCCAGGAATCCTTATTCTCGACGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGCCTCACTGTGCGCGAGACGTTGCGATACACAGC---
                                  GGGAGAAGGCTCAGTCACTCGCA 1137
                                                                  ATTTTTACATGGACTTGACATCAGTGGACACCCAAAGCAGAGAGCGGGAAATAGAAACGT
                                                                                                                                        AGATGCTTGGCTTCTTCAATAACTGTGGTTACCCCTGTCCTGAACATTCCAATCCCTTTG
                                                                                                                                                                         ACATGGTCCAGTATTTCACAGCCATCGGCTACCCCTGTCCTCGCTACAGCAATCCTGCTG
                                                                                                                                                                                                              ACTTCGACAAAATTGCCATCCTGACTTACGGAGAGTTGGTGTTCTGTGGCACCCCAGAGG
                                                                                                                                                                                                                                               TGTTTGATCTGGTCCTCCTGATGACGTCTGGCACCCCCATCTACTTAGGGGCGGCCCAGC
                                                                                                                                                                                                                                                                                  CTCGCAGGGACCGAATTGTGATTGTCACCATCCACCAGCCTCGCTCTGAGCTCTTCCAAC
                                                                                                                                                                                                                                                                                                                   CCAAAGGCAACCGGCTGGTGCTCATCTCCCTCCACCAGCCTCGCTCTGACATCTTCAGGC
                                                                                                                                                                                                                                                                                                                                                      CAACCACAGGACTGGACTGCATGACTGCAAATCAAATTGTCCTTCTCTTGGCTGAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGAGTTTCCATCGCAGCCCAACTCCTTCAGGACCCCAAGGTCATGATGCTAGATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGTGGCGGACCAATGATTGGCAGCTATAATTTTGGGGGAATTTCCAGTGGCGAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTGCGCTGACACCCGCGTGGGCAACATGTACGTGCGGGGGTTGTCGGGGGGTGAGCGCA
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Pred. No. 2.2e-41;
 1119
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1096

1054 1036

976 994 916 814

736 754 676

796

694 616 634 574 499 439 454 379 394

988 874

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The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a cCC disease. The molecules of the invention are also useful for identifying a CCC disease. The molecules of the invention are also useful for identifying CCC culture or mammal which have ABCG5 balypeptide with a compound and CCC measuring ABCG5 biological activity in the cell culture or in mammal. CCC where an increase or decrease in ABCG5 biological activity in the compound that increases or contacted with the compound, identifies a compound that increases or cCC contacted with the compound, identifies a compound that increases or CCC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CCC ABCG5 biological activity respectively. The cell culture or mammal CCC ABCG5 biological activity or level of ABCG5 mRNA, or level of the CCC second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Stimulation of ABCG5 activity is useful for treating or preventing CCC disease. The method of the invention is useful for increasing cholesterol cativity entered activity is useful for increasing cholesterol ascide sequence encodes the hammater abCG5 polypeptide.
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ABK51687
  Query Match
Best Local Similarity
                                                               Sequence 1069
                                                                                            excretion and/or decreasing cholesterol acid sequence encodes the hamster ABCG5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 47; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel mammalian ATP-binding cassette gene 5 polypeptide, nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-416483/44
P-PSDB; AAU96987.
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arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding hamster ABCG5
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Search completed: July 27, 2003, 00:55:37 Job time: 650.803 secs

Run

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AF324495 Mus muscu X478099 Sequence AF351785 Rattus no

Sequence Homo sapi

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Post-processing: Minimum Match 0%
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Hobbs, H.H., Shan, B., Barnes, R. and Tian, H. Abcg5 and abcg8: compositions and methods of use Patent: WO 02081691-A 7 17-OCT-2002;
                                                                                                            AX685735.1 GI:29371744
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC122243 Mus muscu

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OY 601 GCCTTCATTGCCCAGATGCGGCTGCCCAGAACCTTCTCCCAGGCCCAGGCGTGACAAAAGG 660	OY 541 GTGGCCCACGTGCGCCAGCACCAGCTGCTCCCCAACTTGACTGTGCGAGAGAGCCTTG 600	QY 481 AAGTCAGGCCAGATCTGGATCAATGGGCAGCCCAGCTCGCCTCAGCTGGTGAGGAAGTGT 540	OY 421 GGTTGTGGGAGACCTTCCTTAGATGTGATCACTGGCCGAGGTCACGGCGGCAAGATC 480	Oy 361 ATCCAGAACCTAAGCTTCAAAGTGAGAAGTGGGCAGATGCTGGCCATCATAGGGAGCTCA 420	QY 301 CTGGCTCAGTTCAAGATGCCCTGGACATCTCCCAGCTGCCAGAATTCTTGTGAGCTGGGC 360	OY 241 GAGGTCAGAGACCTCAACTACCAGGTGGACCTCGGCCTCTCAGGTCCCTTGGTTTGAGCAG 300	OY 181 TTCTCCTCTGAAAGTGACAACAACAGCCTGTACTTCACCTACAGTGGCCAGCCCAACACCCTG 240	QY 121 GAGAGAGGGCTGCCGAAAAGGGGCCACTCCCCAGGATACCTCGGGCCTCCCAGGATAGATTG 180	OY 61 AAGAGAGCTGCAGGGCCCAGAGCCTGTGGGCCCCATGGCCGGGAAGGCGGCAGAG 120	QY 1 GTGTCCCTGCTCCAGGAAACAGAGTGAAGACACTGGCCCTGGCAGCAGCAGCTGGGTCT 60	Query Match 100.0%; Score 2669; DB 6; Length 2669; Best Local Similarity 100.0%; Pred. No. 0; Matches 2669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SGDKILSAMELDSYPLYAIYLIVIGLSGGFMYLYYVSLRFIKQKPSQDW" BASE COUNT 595 a 768 c 722 g 584 t ORIGIN	ELATREKAĢSLAALFLEKVROLDEFLWKAETROLDEDTCVESSVTFLJOTNOLPSTKM PGAVQRFTTLIRRQISNDFRDLFTLLIHGAEACLMSMTIGFLYFGHGSIQLSFMDTAA LLFMIGALIFFNVILDVISKCYSERAMLYYELEDGLYTTGPYFFAKILGELPEHCAYI IIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALAAAALLFFFHMASFFSNAL	11GSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSSPQLVRKCVAHVROHNQLLPN LTVRETLAF I AQMRLPRIT SQAQRDKREDVI AELTLLRQCADTRVGNWYVRGLSGGER RRVS1GVQLLWWPGILLILDEPTSGLDSFTAHHLVKTLSRLAKGNRLVLISLHQPRSDI FRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDLTSIDRRSREQ	/protein_id="CAD86573.1" //db_xref="GI:29371745" /translation="MAGKAAEERGLPKGATPQDTSGLQDRLFSSESDNSLXFTYSGQP /translation="MAGKAAEERGLPKGATPQDTSGLQDRLFSSESDNSLXFTYSGQP NTLEVRDLNYQVDLASQVPWFEQLAQFKMPWTSPSCQNSCELGIQNLSFKVVSSGQMLA	CDS 1002121 /note="unnamed protein product; human ABCG8 (hABCG8)" /codon_start=1	source 12669 /organism="Homo sapiens" /mol_type="genomic DNA" //dh yrof="syco.0606"
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Kojima, H.,

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AF324494.1 GI:15088539
                                                   AF324494
                                                                                                                                                 CAACGTGAACAATTAAAAATGTATTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Am. J. Hu
21344600
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Pandya, A., Brewer, H.B. Jr.,
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Lu, K., Lee, M.H., Hazard, S.,
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                   GAAAGTGACAACAGCCTGTACTTCACCTACAGTGGCCAGCCCAACACCCCTGGAGGTCAGA
                                                                 GACCTCAACTACCAGGTGGACCTGGCCTCTCAGGTCCCTTGGTTTGAGCAGCTGGCTCAG
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IIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPN
LTVRETLAFIAQAWRLFRTFSQAQRDKRVEDVLAELRLRQCADTRVGNMYVRGLSGGER
RRVSIGVQLLMNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRLVLISLHQPRSDI
FRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDLTSIDBRSREQ
ELATREKAQSLAALFLEKVRDLDDFLMKAETKDLDEDTCVESSVTPLDTNCLPSPTKM
PGAVQQFTTLIRRQISNDFRDLPTLLHGAEACLMSMTIGFLXFGHGSIQLSFMDTAA
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YNSFYLAGGFWIINLSSLWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKWPLGNLTIAV
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1. .2679
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Pred. No. 0;
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Mletinnen,T., Bjorkhem,I., Bruckert,
r., Salen,G., Dean,M., Srivastava,A.
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2410 ATATAGGCAACTGGATATAGGATGGAACTAAGCAATGAATTAGGTAGCTAGACTGT 	Db Cy	TCCGAGACCTGCCCACCCTCCTCATCGAGGCGGAGGCCTGTCTGATGTCAATGACC 1389	1330 TTCCGA
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8-8	Qy Db	GACACCTGTGTGGAAAGCAGCGTGACCCCACTAGACACCAACTGCCTCCCGAGTCCTACG 1269 	1210 GACACC 1201 GACACC
10 10	ОУ	GAAAAAGTGCGTGACTTAGATGACTTTCTATGGAAAGCAGAGACGAAGGATCTTGACGAG 1209 	1150 GAAAAA 1141 GAAAAA
	Qy Db	AGCAGAGAGCAGGAATTGGCCACCAGGGAGAAGGCTCAGTCACTCGCAGCCCTGTTTCTA 1149 	1090 AGCAGA 1081 AGCAGA
	Оу	TGTCCTCGCTACAGCAATCCTGCTGACTTCTATGTGGACCTGACCAGCATTGACAGGCGC 1089 	1030 TGTCCT 1021 TGTCCT
2050 AGCGGTGGCTTCATGGTCCTGTACTACGTGTCCTTAAGGTTCATCAAACAGAAACCAAGT	Оу	CCCATCTACTTAGGGGCGGCCCAGCACATGGTCCAGTATTTCACAGCCATCGGCTACCCC 1029	970 CCCATC 961 CCCATC
1990 AGTGCCATGGAGCTGGACTCGTACCCTCTACGCCATCTACCTCATCGTCATTGGCCTC	Оy	CAGCCTCGCTCTGACATCTTCAGGCTGTTTGATCTGGTCCTCCTGATGACGTCTGGCACC 969	910 CAGCCT 901 CAGCCT
8 - 8	Оу	CTGGTGAAGACCTTGTCCAGGCTGGCCAAAGGCAACCGGCTGGTGCTCATCTCCCTCC	850 CTGGTC 841 CTGGTC
	Оу	CCAGGAATCCTTATTCTCGACGAACCCACCTCTGGGCTCGACAGCTTCACAGCCCACAAC 849	790 CCAGGA 781 CCAGGA
7 - 7	Оу Db	CGGGGGTTGTCGGGGGGTGAGCGCAGGAGAGTCAGCATTGGGGTGCAGCTCCTGTGGAAC 789	730 CGGGGG 721 CGGGGG
	Оу	GTGATCGCGGAGCTGCGGCTTAGGCAGTGCGCTGACACCCGCGTGGGCAACATGTACGTG 729	670 GTGATO
1690 CACTTCCTGCTGGTGGCTGGTGGTCTTCTGTTGCAGGATTATGGCCCTGGCCGCGGG 	Оу	GCCCAGATGCGGCTGCCCAGAACCTTCTCCCAGGCCCAGGCGTGACAAAAGGGTGGAGGAC 669	610 GCCCAC 601 GCCCAC
	Db Oy	GTGCGCCAGCACAACCAGCTGCTCCCCAACTTGACTGTGCGAGAGAGA	550 GTGCGG 541 GTGCGG
1570 CCATATTTCTTTGCCAAGATCCTCGGGGAGCTTCCGGAGCACTGTGCCTACATCATCATC	Qy Db	CAGATCTGGATCAATGGGCAGCCCAGCTCGCCTCAGCTGGTGAGGAAGTGTGTGGCCCAC 549	490 CAGATO 481 CAGATO
	Дy	AGAGCCTCCTTGCTAGATGTGATCACTGGCCGAGGTCACGGCGGCAAGATCAAGTCAGGC 489	430 AGAGCO 421 AGAGCO
	Qy Db	CTAAGCTTCAAAGTGAGAAGTGGGCAGATGCTGGCCATCATAGGGAGCTCAGGTTGTGGG 429 	370 CTAAG 361 CTAAG
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Berge, K.E., Tlan.H., Graf, G.A., Yu.L., Gr Kwiterovich, P.; Shan, B., Barnes, R. and Ho Accumulation of Dietary Cholesterol in Si Mutations in Adjacent ABC Transporters Science (2001) In press
2 (bases 1 to 2022)
Berge, K.E., Tlan.H., Graf, G.A., Yu.L., Gr Kwiterovich, P., Shan, B., Barnes, R. and Ho hteat Submitsein
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SGDKILSVMELDSYSDYAYAIYLUVIGLAGGFMVLXYYSLRFIKQKPSQDW*
24 a 603 c 545 g 450 t
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                                                                                                                                                                                                                                                  /note-"ATP-binding
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Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae
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d Hobbs,H.H.
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Hobbs, H.H.
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 0240541-A 29 23-MAY-2002; Incyte Genomics, Inc. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/mol_type="genomic DNA"
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/db_xref="ftaxon:9606"
/note="Incyte ID No: 6585710CB1"
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Submitted (21-FEB-2001) Division of Endocrinology, Diabetes
Medical Genetics, Medical University of South Carolina, 114
St. STB 541, Charleston, SC 29407, USA
4 (bases 1 to 4829)
Lu.K., Yu.H., Lee,M. and Patel,S.B.
Direct Submission
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Lu,K., Yu,H., Lee,M. and Patel,S.B.
Molecular cloning, genomic structure, and characterization
mouse head to-head tandem ABC transporters
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Lu,K., Lee,M.H., Hazard,S., Brooks-Wilson,A., Hidaka,H., Kose,L., Stalenhoef,A.F., Mietinnen,T., Bjorkhem,I., Brucke Pandya,A., Brewer,H.B. Jr., Salen,G., Dean,M., Srivastava,
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 Score 1518.6;
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2259 CAGTGGCACAGACCAGCACAGGATGGCAGTAGAATAAAGACAGTCGAAAGGGATTTCTG 2318	2199 CTGGGGACAGTGAGGACATGACCCTACAGATGCTCAGCTACATCCGGCCCAGGGTGCTG 2258	2139 CCCGCTGGTGGGGACCTGAGCAGACCCTTCAACTGCACTCCCTCAGGAGCCCCTTC 2198	8 7	2019 CTACGCCATCTACCTCATCGCCTCAGGCGCTGGCTTCATGGTCCTGTACTACGT 2078	1959 CACCATCGCGGTCTCAGGAGATAAAATCCTCAGTGCCATGGAGCTGGACTCGTACCCTCT 2018	1899 TGAAGGGCTGATGAAGATTCAGTTCAGCAGAAGAACTTATAAAATGCCTCTCGGGAACCT 1958	1839 GAGCAGCCTGTGGACAGTGCCCGCGTGGATTTCCAAAGTGTCCTTCCT	1779 CTTCTTCAGCAATGCCCTCTACAACTCCTTCTACCTCGCCGGGGGCTTCATGATAAACTT 1838							1359 TGGGCGGAGCCTGTCTGATGTCAATGACCATGGCCTTCCTCTATTTTGGCCATGGGAG 1418		ALAMAK-KACHAKTISCOTICGAKI TOTTAGGAKARTIGCOTIGGGGGGTGGAGGATTTAG	GINGAAAGUTGAGGCAAAAGAGTUTCGACACAGGCACCTATGCAGTCAGCCAGACCCTCAC

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DDASQGLQDSLESSESDNSLYETYSGQ WRSHSSQDSCELGTRNLSFKVRSGQML						South Carolina, 114 Doughty A	crinology, Diabetes and			lving sterolin-1 and respectively	se sitosterolemia: genomic	, Bjorkhem,I., Bruckert,E., Dean,M., Srivastava,A. and	n,A., Hldaka,H., Kojima,H.,	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.			NA linear ROD 07-AUG-2001 complete cds.			÷	AATGTCCTCTCTTATCTCTGTG: 2573	GATGCCATCCTTCTTTTGTG 2618	GCCCCACACTCCGTGGTGAGCC 2558			TATATCTCTATATAAACAACCCAGTATGGAATGGGAAC 2402	CAACTCGATATAGGATGGGAGC 2438	AAACAGGTACTTCGTGAACCTGTAACG 2350		AGACAGTTGAGAGGTTTCTG 2303
876 881	Qy 816 CACCTCTGGGCTCGACAGC Db 821 CACTTCTGGCCTCGACAGC	Db 761 ACGAGTGAGCATTGGGGTG	Qy 756 GAGAGTCAGCATTGGGGTG	Db 701 GTGCGCCAACACCGGGGTG	641		Db 581 CAACCTGACCGTCAGAGAC	TTGACTGTGC	Db . 521 TACGCCTCAGCTGGTGAGC			456	Db 401 GATGCTGGCCATCATAGGC	396	Qy 336 CTGCCAGAATTCTTGTGTGTA 1 <td>187</td> <td></td> <td></td> <td>Qy 216 CTACAGTGGCCAGCCCAAC</td> <td> QY</td> <td>150 CATGG</td> <td>. 99</td> <td>Best Local Similarity 77.0%; Matches 1965; Conservative</td> <td>Match .</td> <td>BASE COUNT 870 a 1023 c</td> <td>YNSEYLTAGEN</td> <td>PGMIEGFSTLEFF</td> <td>IFRLFDLVLLM REVATVEKAQSI</td> <td>NLTVRETLAFI RRRVSIGVOLLI</td> <td>AIIGSSGCGRAS</td>	187			Qy 216 CTACAGTGGCCAGCCCAAC	QY	150 CATGG	. 99	Best Local Similarity 77.0%; Matches 1965; Conservative	Match .	BASE COUNT 870 a 1023 c	YNSEYLTAGEN	PGMIEGFSTLEFF	IFRLFDLVLLM REVATVEKAQSI	NLTVRETLAFI RRRVSIGVOLLI	AIIGSSGCGRAS

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YAGFMINLDNLMIVPAMISKLSFLRMCFSGLMQIQFNGHLYTTQIGNETFSI
SAMDLNSHPLYAIYLLVIGISYGFLFLYYLSLKLIKQKSIQDM*
3 C 932 9 849 t

Score 1511.6; Pred. No. 0; 0; Mismatches DB 10; Length 3674;

CAGAGGAGAGAGGGCTGCCGAAAGGGGCCACTCCCCAGGATAC 158 TTGAGCAGCTGGCTCAGTTCAAGATGCCCTGGACATCTCCCAG ACACCCTGGAGGTCAGAGACCTCAACTACCAGGTGGACCTGGC 275 ATAGATTGTTCTCCTCTGAAAGTGACAACAGCCTGTACTTCAC 215 534; Indels Gaps 395 335 340 220 8

GGAGCTCAGGTTGTGGGAGAGCCTCCTTGCTAGATGTGATCAC

GAGCTCAGGCTGCGGGAGAGCCTCACTACTCGACGTGATCAC

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GCAAGATCAAGTCAGGCCAGATCTGGATCAATGGGCAGCCCAG CAAGATGAAATCAGGACAAATTTGGATAAATGGGCAACCCAG

GGAAGTGTGTGGCCCCACGTGCGCCCAGCAACCAACCAGCTGCTCCC GAAGTGCGTTGCGCATGTGCGGCAGCATGACCAACTGCTGCC

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695 640 635 580 575 520 515 460

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ACAAAAGGGTGGAGGACGTGATCGCGGAGCTGCGGCTTAGGCA |CAAACGGGTGGAAGACGTAATCGCCGAGCTGCGGCTGCGGCA

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                                 CTTCACCTTCTCCATCCTCGGAGACACGATGATCAGTGCCATGGACCTGAACTCGCATCC
                                                  CCTCACCATCGGGGTCTCAGGAGATAAAATCCTCAGTGCCATGGAGCTGGACCTCGTACCC
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AY196216
                                                            Direct Submission
Submitted (12-DEC-2002) The Jackson
Bar Harbor, ME 04609, USA
                                                                                                               2 (bases 1 to 2284)
Lyons, M.A., Wittenburg, H.,
                                                                                                                                    Unpublished
2 (bases 1
                                                                                                                                                              Mice
                                                                                                                                                                          Primary Roles of FXR and Susceptibility: Evidence
                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2284)
                                                                                                                                                                                                                                                                                                                                                   AY196216 2284 bp mRNA linear Mus musculus strain PERA/Ei ATP-binding cassette member 8 (Abcg8) mRNA, complete cds.
                                                                                                                                                                                                         Paigen, B.
                                                                                                                                                                                                                   Wittenburg, H.,
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/mol_type="mRNA"
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                                                         Location/Qualifiers
                            /organism="Mus musculus"
                                             . 2284
                                                                                                                                                                                                                   Lyons, M.A., Li, R.,
                                                                                                                                                                       ABCG5/ABCG8 in Cholesterol Gallstone from a Cross of PERA/E1 and I/Ln Inb.
                                                                                                                  Walsh, K.A.,
                                                                                                                                                                                                                                                Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                   Churchill, G.A.,
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                                                                                     Laboratory,
                                                                                                                Carey, M.C. and Paigen, B.
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Carey, M.C.

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                                    GCCTCAGCTGGTGAGGAAGTGTGTGGCCCACGTGCGCCAGCACAACCAGCTGCTCCCCAA
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NTLEVURDLTYQYDIASGVPWFEGLAGFKLPWRSHSSGOSEGGIRNLSFKYRSGONLA
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LTVRETLAFIAQWRLPRTFSQAQRDKRVEDVIAELRLQCANTRKGUNTYVGEYSGGER
RRVSIGVQLLMNPGILILDEPTSGLDSFTAHNLYTTLSRLAKGNRLYLISLHQPRSDI
FRLFDLVLLMTSGTPIYLGAAQQWQYETSIGHPCPRYSNPADFYVDLTSSIDRRSKER
EVATYEKAQSLAALFLEKYQGFDDFLMKAEAKELNTSTHTYSLTLTQDTDCGTAVELP
GMIEQFSTLIRRQISNDFTDLFFLIHGSEACLMSLIIGFLYYGGBAKQLSFMOTAAL
LFMIGALIPFNVILDWYSKCHBERSMLYYELEDGLYTAGPYFFAKILGELPEHCAYVI
IYAMPIYWLTNLRPVPELFLLHFLYWILVVCCKTMALASAMLDTFHMSSFFCNALY
NSFYLTAGFMINLDNLWIVPAMISKLSFLRWCFSGLMQIQFNGHLYTTQIGNFTFSIL
GDTMISAMDLNSHPLYAIYLIVIGISYGFLFLXYLSKLIKQKSIQDW"

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102. :2120
/gene="Abcg8"
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/protein_id="AAO45096.
/db_xref="GI:31322262"
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white subfamily"
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/map="55 cM"
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/chromosome="17"
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79.8%;
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                                                                                                                       /mol_type="mRNA"
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          /gene="Abcg8"
                         /tissue_type="liver"
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IIGSSGCGRASLLDVITGRGHGGKMKSGQIWINGQPSTPQLVRKCVAHVRQHDQLLPN
LTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQCANTRYGNTYVRGVSGGER
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/note="ATP-dependent canalicular
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/protein_id="AAO45095.
/db_xref="GI:31322260"
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                           CTTCTTCTGCAATGCCCTCTACAACTCCTTCTACCTTACCGCCGGCTTCATGATAAACTT
                                                                                     CTTCTTCAGCAATGCCCTCTACAACTCCTTCTACCTCGCCGGGGGCTTCATGATAAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hobbs, H.H., Shan, B., Barnes, R. and Tian, H. Abcg5 and abcg8: compositions and methods of use Patent: WO 02081691-A 3 17-CCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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Mammalia; Eutheria; Rodentia;
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                                                LFMIGALIPFNVILDVVSKCHSERSMLYYELEDGLYTAGPYFFAKILGELPEHCAYVI
IYAMPITWLTNLARVPELEFLLHFLLVMLVVFCCCFTMALAASAMLPTFHHSSEFCNALY
NSFYLTAGFMINLDNLMIVPAMISKLSFLRWCFSGLMQIQFNGHLYTTQIGNFTFSIL
GDTMISAMDLNSHPLYAIYLIVLGISYGFLFLYYLSLKLIKQKSIQDW*
3 598 c 510 g 467 t
                                                                                                                              RRVS.TCVQLLMNPGILILDEPTSGLDSFTAHNLVTTLSRLAKGNRLVLISLHQPRSDI
FRLFDLVLLMTSGTPIYLGAAQQMVQYFSIGHEVRYSDFAPYVDLTSIDRRSKER
FRLFDLVLLMTSGTPIYLGAAQQMVQYFSIGHEVRYSTTUSLTLTQDTDCGTPAVEL
EVATVEKAQSLAALFLEKVQGFDDFHMKAEAKELNTSTHTVSLTLTQDTDCGTPAVEL
GMIBQFSTLIRRQISNDFRDLPTLLIHGSEACLMSLIIGFLYYGHGAKQLSFMDTAAL
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NTLEVRDLTYGVDIASGVPWFEGLAGFKIPWHSSGDSCELGIRLSFKVRSGQMLA
IIGSSGCGRASLLDVITGRGHGKMKKSGQIWINGQPSTPDLVRKCVAHVRQHDQLLP
LTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQCANTRVGNTYVRGVSGGER
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                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:10090"
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/db_xref="GI:29371741"
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                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; mouse ABCG8
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1060 TATGTGGACCTGACCAGCATTGACAGGCGCAGCAGAGAGAG			TCTGGGCTCGACAGCTTCACAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGGCCAAA 8	D 601 GCCAACACCAGAGTGGGCAACACGTATGTACGTGGGGTGTCCGGGGGTGAGCGCCGACGA 660 Y 760 GTCAGCATTGGGGTGCAGCTCCTGTGGAACCCAGGAATCCTTATTCTCGAACGAA	541 700	TGTGCGAGAGACCTTGGCCTTCATTGCCCAGAT	DY 520 CCTCAGCTGGTGAGGAAGTGTGTGGCCCACGTGCGCCAGCACAACCAGCTGCTCCCCAAC 579	Dy 460 CGAGGTCACGGCGGCAAGATCAAGTCAGGCCAGATCTGGATCAATGGGCAGCCCAGCTCG 519	29 400 CTGGCCATCATAGGGAGCTCAGGTTGTGGGAGAGCCTCCTTGCTAGATGTGATCACTGGC 459	Dy 340 CAGAATTCTTGTGAGCTGGGCATCCAGAACCTAAGCTTCAAAGTGAGAAGTGGGCAGATG 399	OY 280 CAGGTCCCTTGGTTTGAGCAGCTGGCTCAGTTCAAGATGCCCTGGACATCTCCCAGCTGC 339	Oy 220 AGTGGCCAGCCCAACACCCTGGAGGTCAGAGACCTCAACTACCAGGTGGACCTGGCCTCT 279	OY 160 TCGGGCCTCCAGGATAGATTGTTCTCCTCTGAAAGTGACAACAGCCTGTACTTCACCTAC 219	OY 100 ATGGCCGGAAGGCGGCAGAGAGAGAGGGCTGCCGAAAAGGGGCCACTCCCCAGGATACC 159	Best Local Similarity 82.0%; Pred. No. 5.3e-306; Matches 1659; Conservative 0; Mismatches 360; Indels 3; Gaps 1;
RESULT 10 AC084265 AC084265 LOCUS AC084265 AC084265 LOCUS DEFINITION Homo sapiens chromosome 2, clone CTB-2367F13, complete sequence. ACCESSION AC084265 VERSION AC084265 4 GI:17488659	Db 1918 TATGCGATCTACTCATTGTCATCGGCATCAGGCTACGGCTTCCTGTTCCTGTACTATCTA 1977 2080 TCCTTAAGGTTCATCAAACAGAAACCAAGTCAAGACTGGTGA 2121	OY 1960 ACCATCCCGGTCTCAGGAGATAAAATCCTCAGTGCCATGGAGCTGGACTCGTACCCTCTC 2019	1900 1798	1840 AGCAGCCTGTGGACAGTGCCCGGGTGGATTTCCAAAGTGTCCTTCCT	Db 1618 TGCTGCAGGACCATGGCCTGGCTGCCTTGCCACCTTCCACATGTCCTCC 1677 Qy 1780 TTCTTCAGCAATGCCCTTACAACTCCTTGTACCTCGCGGGGGTTCATGATAACTTG 1839	Db 1558 CTGCGGCCCTGCCCTGCCCCCCCCCCCCCCCCCCCCCC	1600 CTTCCGGAGCACTGTGCCTACATCATCATCTACGGGATGCCCACCTACTGGCTGG		11 14 13 4	QY 1420 ATCCAGCTCTCATGATACAGCCGCCCTCTTGTTCATGATCAGTGCTCTCATCCCT 1479	QY 1360 GGGCCGAGGCCTGTCTGATGTCAATGACCATCGCCTTCTCTCTATTTTGGCCATGGGAGC 1419	QY 1300 ACGCTGATCCGTCAGATTTCCAACGACCTCCGAGACCTGCCCACCCTCCTCATCCAT 1359	QY 1240 CTAGACACCAACTGCCTCCCGAGTCCTACGAAGATGCCTGGGGCGGTGCAGCAGCTTTACG 1299	Db 1081 TGGAAAGCASAGGAAGTCTTGACGAGGACCCTGTGTGGAAAGCAGCGTGACCCCA 1239 1081 TGGAAAGCTGAGGCAAAGGAACTCAACACAAGCACCCACACAGTCAGCCTGACCCTCACA 1140	1021 A

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                                                                                                                                                                                                                                                                                                                         Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Ianazarae, B., Index, M., Karatas, A., Kells, C., Larocque, K., Ianazarae, B., Index, M., Karatas, A., Kells, C., Larocque, K., Ianazarae, B., Index, M., Karatas, A., Kells, C., Larocque, K., Ianazarae, B., Index, M., Karatas, A., Kells, C., Larocque, K., Ianazarae, B., Index, M., Karatas, A., Kells, C., Larocque, K., Ianazarae, B., Ianazarae, B., Ianazarae, M., Karatas, A., Kells, C., Larocque, K., Ianazarae, B., Ianazarae, M., Ianazae, M., Ianazae, M., Ianazarae, M., Ianazae, M., Ianaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-AUG-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 127066)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Boguslavkty,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cook,B., Cook,
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Chang, J., Cook, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Chang, J., Chazaro, B., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Chang, J., Chazaro, B., Chang, J., Chazaro, Chang, J., Chazaro, B., Chang, J., Chazaro, Chang, J., C
                                                                                                                                                                Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G. MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews
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                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 127066)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Kells, C., LaRocque,
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complement(12221. .12282)
                                                                                                                                                                                                                                 _family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                  family-"AT_rich"
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Strauss, N., Subramanian, A., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P Topham,K., Travers,M., Travis,N., Trigilio,J., Vassillev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Direct Submission Seaman,S., Severy,P., ., Rosetti, M., Roy, A., (11-DEC-2001) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA 2001 this sequence version replaced gi:15284200. ., Zembek,L., Zimmer,A. and Zody,M. Spencer, B., Stange-Thomann, N., Stojanovic, N., an, A., Talamas, J., Tesfaye, S., Theodore, J., Santos, R., Schauer, S., Schupback, R.,

Contact: sequence_submissions@genome.wi.mit.edu Center clone name: 2367_F_13 Center project name: Web site: http://www-seq.wi.mit.edu Center: Whitehead Institute/ MIT Center for Genome Research

Genome Center

complement(469. /clone_lib="CITB Human complement(8. .170) complement(469. .516)
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1994 CCATGGAGCTGGACTCGTACCCTCTACCGCATCTACCTCATCGTCATTGGCCTCAGCG 2053
                                                                                                     1961 CCATCGCGGTCTCAGGAGATAAA----------
                                                                                                                                      CCATCGCGGTCTCAGGAGATAAAGTAAGCGGGGGAAGGCCTCGGGTTCTAAATTATTGGAC 59677
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/rpt_family="MER115"
complement(22843. .22942)
/rpt_family="MER115"
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/rpt_family="LTR37B"
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complement(13160)
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lement/1500)
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_family="Aluy"
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lement(14184. .14250)
_family="L2"
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lement(17911. .1
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lement(16988. .17104)
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Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,
Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 20, 2002 this sequence version replaced g1:25046635.
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, E Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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/clone_lib="RPCI-11 Human
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                                                                                                                  Direct Submission
Submitted (16-APR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 29, 2002 this sequence version replaced gi:18767626.
                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (20-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
5 (bases 1 to 139342)
                                                                                                                                                                                                                          Submitted (29-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA 6 (bases 1 to 139342)
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4 (bases 1 to 139342)
Waterston, R.H.
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Submitted (27-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Harkins,C., Haakenson,W. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-1413K20
Unpublished (2001)
3 (bases 1 to 139342)
Waterston,R.H.
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Genome Res. 8 (11), 1097-1108 (1998)
99063792
                                                                                                                                                                                                                                                                                               Waterston, R.H.
Direct Submission
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AC108476.5 GI:19807988
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                                                                                                                                                                                                                        63108, USA
(bases 1 to 139342)
                 Contact: sapiens@watson.wustl.edu
Center project name: H_NH1413K20
                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                    Web site: http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                         Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality 30); an attempt was made to resolve all sequencing problems, suc

as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org VECTOR: pBACe3.6 Zhao, B., Frengen, E.,

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-489K22, 2000 bp overlap.
Actual end is at base position 139342 of RP11-1413K20.

The region between 132012 and 132017 is covered only by a pcr

		misc_feature 4099.	/note misc_feature 4099.	misc_feature 3044.		/note misc_feature 2983.	misc_feature 2983:	/note repeat_region 2234.	/rpt_ misc_feature 1867.	repeat_region 847	/nc ye5	/not misc_feature 706.	misc_feature 706.	/nc	/note misc_feature 372.	misc_feature 318	misc_reature 93.		misc_feature 93.	misc_feature 93.	misc_feature 55.	/c <u>.</u>	/ma	/c}	/mc		FEATURES LOC SOURCE 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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ATCCTCAGTG

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1983

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58331

2293

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58091 2113 58031

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ORGANISM	-	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	F351812S13	KESOLT LS
Homo sapiens (human)	13 of 13		AF351824.1 GI:15146443	AF351824	Homo sapiens sterolin-2 (ABCG8) gene, exon 13 and complete cds.	F351812S13 2201 bp DNA linear PRI 10-AUG-2001		

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1 (bases 1 to 2201)

Lu,K., Lee,M.H., Hazard,S., B

Ose,L., Stalenhoef,A.F., Miet
Pandya,A., Brewer,H.B. Jr., S
Patel,S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-FEB-2001) Division of Endocrinology, Diabetes and Medical Genetics, Medical University of South Carolina, 114 Doughty St, STB 541, Charleston, SC 29403, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Two genes that map to the STSL locus cause sitosterolemia: gestructure and spectrum of mutations involving sterolin-1 and sterolin-2, encoded by ABCG5 and ABCG8, respectively Am. J. Hum. Genet. 69 (2), 278-290 (2001)
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                                                                          /number=13
a 536 c
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NTLEVEDLNCQVDLASQVPWFEQLAOFKMPWTSPSCONSCELGIONLSFKVRSGQNLA
IIGSSCCGRASLLDVTGRGHGKIKSGQIMINGOPSSPOLVPKCVAHVRGHNQLLPN
LTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAELRLRQCADTRVGHNYVRGLSGGER
RRVSIGVQLLMNPGILLIDEFTSGLDSFTAHHLVRTLSCLAFGNRLVALISLHQPRSDI
FRLFDLVLLMFSGTPTYLGAAQHNVQYFTAISCPCRYSUPADFYVDLTSIDRRSRG
ELATREKAQSLAALFLEKVRDLDFLLHRAETKDLDEDTCVESVTPLOTNCLESSTKMP
GAVQQFKTLIRRQISNDFRDLFTLLHGAEACLMSHTIGFLYFGHGSIQLESPTAAL
GAVQQFKTLIRRQISNDFRDLFTLLHGAEACLMSHTIGFLYFGHGSIQLESPTAAL
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AF351014.1:924. .1080,AF351815.1:674. .912,
AF351816.1:121. .253,AF351817.1:66. .335,AF351818.1:1.
AF351819.1:48. .128,AF351820.1:310. .509,
AF351821.1:243. .319,AF351822.1:101. .368,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Join(AF351812.1:<1227. .1289,AF351813.1:3941. .4042,

AF351814.1:924. .1080,AF351815.1:674. .912,

AF351816.1:121. .253,AF351817.1:66. .335,AF351818.1:1.

AF351819.1:48. .128,AF351820.1:310. .509,

AF351821.1:243. .319,AF351822.1:101. .368,

AF351823.1:699. .816,45. .>182)
                                                                                                                                                                                                    IYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALAAAALLPTFHMASFFSNALY
NSFYLAGGEMINLSSLWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVS
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order(AF351812.1:<1.271...2809,AF351813.1:1...4665,
AF351814.1:1...2368,AF351815.1:1...1323,AF351816.1:1...300
AF351817.1:1...660,AF351818.1:1...203,AF351819.1:1...888,
AF351820.1:1...685,AF351821.1:1...884,AF351822.1:1...1292,
                                                                                                                                                                             GDKILSAMELDSYPLYAIYLIVIGLSGGFMVLYYVSLRFIKQKPSQDW'
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                                                                                                                               /gene="ABCG8"
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/db_xref="GI:15146444"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="between D2S2294 and D2S2298"
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/mol_type="genomic DNA"
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Two genes that map to the STSL locus cause sitosterolemia: structure and spectrum of mutations involving sterolin-1 ar sterolin-2, encoded by ABGG5 and ABGG8, respectively Am. J. Hum. Genet. 69 (2), 278-290 (2001)
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 660)

Lu,K., Lee,M.H., Hazard,S., Brooks-Wilson,A., Hidaka,H., Kojima,H. Ose,L., Stalenhoef,A.F., Mietinnen,T., Bjorkhem,I., Bruckert,E., Pandya,A., Brewer,H.B. Jr., Salen,G., Dean,M., Srivastava,A. and
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Ar351817
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278-290 (2001)

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Direct Submission

Submitted (21-FEB-2001) Division of Endocrinology, Diabe
Medical Genetics, Medical University of South Carolina,
St, STB 541, Charleston, SC 29403, USA

Location/Qualifiers
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                                         Patel, S.B.

Two genes that map to the STSL locus cause sitosterolemia: genomic structure and spectrum of mutations involving sterolin-1 and sterolin-2, encoded by ABCG5 and ABCG8, respectively ABC, J. Hum. Genet. 69 (2), 278-290 (2001)
                                                                                                         Lu,K., Lee,M.H., Hazard,S., Brooks-Wilson,A., Hidaka,H., Kojima,I
Ose,L., Stalenhoef,A.F., Mietinnen,T., Bjorkhem,I., Bruckert,E.,
Pandya,A., Brewer,H.B. Jr., Salen,G., Dean,M., Srivastava,A. and
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11452359
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/Clone="1081G2; 32814"
/cell_type="ES cell"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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St, STB 541, Charleston, SC
Location/Qualifiers
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/clone="1081G2; 32814"
/cell_type="ES cell"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Search completed: July 27, 2003, 05:52:39 Job time: 9494.57 secs

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       Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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A1151811 u146c10.y
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CB502603 ssa1mge50
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BG29953 HYSMEB001.g
CB682737 OSJNEE111
BZ614705 1946b01.g
CB682737 OSJNEE111

	ALIGNMENTS
171	
TION	AK004871 3623 bp mRNA linear HTC 05-DEC-2002
1	library, clone:1300003C16 product:ATP-BINDING CASSETTE, SUB-FAMILY
	G, MEMBER 8 (STEROLIN-2) homolog [Mus musculus], full insert sequence.
NOI	AK004871
Ż	AK004871.1 GI:12836380
DS	HTC; CAP trapper.
	Mus musculus (house mouse)
MSIN	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia: Sciurognathi, Muridae, Vertebrata;
NCE	1
ORS	Carninci, P. and Hayashizaki, Y.
Ħ	High-efficiency full-length cDNA cloning
NAL	Meth. Enzymol. 303, 19-44 (1999)
INE	99279253
MED	10349636
NCE	N .
ORS	Carninci, P., Shibata, Y., Hayatsu, N., Suqahara, Y., Shibata, K.,
	Itoh, M., Konno, H., Okazaki, V. Miramatan M. and Ususchinati

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COMMENT
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I 6 II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)
6 (bases 1 to 3633)
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Fax:81-45-503-9216)
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CTCTCAGGTCCCTTGGTTTGAGCAGCTGGCTCAGTTCAAGATGCCCTGGACATCTCCCCAG
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                                  CTGCCAGAATTCTTGTGAGCTGGGCATCCAGAACCTAAGCTTCAAAGTGAGAAGTGGGCA 395
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SNTLEVRDLTYQVDIASQVFWFEQLAQFKIFWRSHSSQDSCELGIRNLSFKVRSGQML
AIIGSSGCGRASLLDVITGRGHGGKWKSGQIWINGQPSTPQLVRKCVAHVRQHDQLLP
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PGMIEQFSTLIRRQISNDFRDLPTLLIHGSEACLMSLIIGFLYYGHGAKQLSFMDTAA
LLFMIGALIPFNVILDVVSKCHSERSMLYYELEDGLYTAGPYFFAKILGELPEHCAYV
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LGUTMISAMDLNSHPLYAIYLIVIGISYGFLFLYYLSLKLIKQKSIQDW*
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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CAGGGGCCCCACACE	AGGAATTGTTGGAAG AGAAATTTCTGGAAG	ATAGGCAACTCGAT. TAAACAACCCAGT	AACCTGCACTCGGT	AATAAAGACAGTCG AATAAAGACAGTTG	CTCAGCTACATCCG	CTGCACTCCCTCCT GGCTGGCCACCCC	AGACTGGTGATTCA AGACTGGTGATACT	CGÉTGGCTTCATGG CTACGGCTTCCTGT	TGCCATGGAGCTGG	AACTTATAAAATGC	CAAAGTGTCCTTCC	CCTCGCCGGGGGCT	CATGCTGCCCACCT	ACTTCCTGCTGGTGT ALLELELELELELE ACTTCCTGCTCGTGT	ACGCGATGCCCACCT	CATATTTCTTTGCCA 	45 TCCTTTCAATGTCATCCTGGATGTCGTCTCCAAATGTCACTCGGAGAGGTCAATGCTGTA
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	1416 GAGCATCCAGCTCCTTCATGGATACAGCCGCCCTCTTGTTCATGATCGGTGCTCCAT 1475	1356 CCATGGGCCGGAGGCCTGTCTGATGTCAATGACCATCGGCTTCCTCTATTTTGGCCATGG 1415	1296 TACGACGCTGATCCGTCAGATTTCCAACGACCTCCTGCCCCTCCTCAT 1355	1236 CCCACTAGACACCAACTGCCTCCCGAGTCCTACGAAGATGCCTGGGGGGGTGCAGCAGTT 1295	1176 TCTATGGAAAGCAAGGATCTTGACGAGGACCTGTGTGGAAAGCAGCGTGAC 1235	1116 GGAGAAGGCTCAGTCACTCGCAGCCCTGTTCTAGAAAAAGTGCGTGACTTAGATGACTT 1175	1056 CTTCTNTGTGGACCTGACCAGCAGTGACAGGGGCAGCAGAGAGAGA	996 CATGGTCCAGTATTTCACAGCCATCGGCTACCCCTGTCCTGCTACAGCAATCCTGCTGA 1055	936 GPTTGATCGGTCCTCGATGACGTCTGCCACCCCATCTACTTAGGGGGGGG	### SCANAGGAACGGCTGGTGCTCACAGCCTGGCTCTGACATCTTCAGGCT 935 ####################################	### 1816 CACCTETIGGGCTTCACAGCCCACAACCTGCTGAAAACCTTGTCCAGGCTGGC #75 ### 1111111111111111111111111111111111	756 GARAGICAGACATICGAGACCAGGAMACCTTANTICGAGAACC 815 728 ACGASTGAGACTCGACAGCTTCACAGGACCCAGGAMACCTTANTICGAGAGAACC 815 728 ACGASTGAGCATTGGAGTTCACAGCTCCAGGAMACCTGATTCGATTGAACC 875 816 CACCTTGGGGTGCACAGCTTCACAGCTCCAGGAMACCTGATTGATTCGATTGAACC 877 817 CAMAGGCAACCTGACAACCTTCACAGCCCACAACCTGGTGATGAACCTTGTCCAGCTGGG 877 818 CACTTCTGGCCTCGACAACCTTCACAGCCCACAACCTTGTCCCCCCCAGGATTCTCCAGCTTGGC 877 819 CATITGACTGGTCCTCCTCACAGCCCACAACCTTGTCCCCCTCCACACCTTGTCCCGCCTGGG 847 810 CAAAGGCAACCGCTGGTCATCTCCTCCACACCCCCCACACCTTGTCCCGCCTGGG 847 811 CAAAGGCACAACCTGGTCTCTCTGATGACACCTGGCTGGC	696 GERCECTRANACCOCONGROGECANANTECTRACTGGGGGGGTTCAGGGGGTGAGCGCAG 755 611 111	615 CTCCCAGGCCAGCCCACCANANAGGTGGGGACTGACGCGGCTGCGGGCTGGCGGCACCACCACCACCACCACCACCACCACCACCACCA	516 CANCTEGACIONACCORCOCANAGACCTEGACCOCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCTCCCCCANAGACCCCCANAGACCCTCCCCCANAGACCCCANAGACCCCANAGACCCCANACACCCCCANAGACCCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCANAGACCCCCANAGACCCCANAGACCCCANAGACCCCCACCACCCCCACCAACCCCCCACCAACCCCCCACCAACCCC	1516 CTICCACCACCACCACCACACACACTACACCACACACCACACACACACACACCAC	456 TRICCOLOGICACCOCCACAMATCHACTCACCAMATCHACTACCACCACT 151

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                                                                                                                                                                                                                                                                                                 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwâld, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-cka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus
    The FANTOM Consortium and
                                                                                                                    Nature 409
21085660
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Mammalia; Eutheria;
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                                                                                                                                                    annotation of a full-length mouse cDNA collection (6821), 685-690 (2001)
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kiyama,J., Nishi,K.,
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Exploration
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                                                                                                                                                                                                                                                                                                   244 TGAAATCAGGACAAATTTGGATAAATGGGCAACCCAGTACGCCTCAGCTGGTGAGGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2417)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222
Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., (
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL:http://genome.gsc.riken.go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site for further details.
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                                                                                      TGGCCTTCATTGCCCAGATGCGGCTGCCCAGAACCTTCTCCCCAGGCCCAGCGTGACAAAA
                                                                                                                                                                                                               GTGTGGCCCACGTGCGCCAGCACCAGCTGCTCCCCAACTTGACTGTGCGAGAGACCT
   GGGTGGAGGACGTGATCGCGGAGCTGCGGCTTAGGCAGTGCGCTGACACCCGCGTGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FANTOM_DB:D030040P06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="9 days embryo'
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76.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1286.2;
Pred. No. 1.3e
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.3e-308;
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1619 ACATCATCATCTACGGATGCCCACCTACTGGCCGACCTGACGCCAGGCCTACAGCCTCAGC 1678		1 9 2 9 1		1079 TTGACAGGCGCAGCAGAGAGAGAGAGACACCAGGAGAAAGGCTCAGTCAG	7 959 CGTCTGGCACCCCATCTACTTAGGGGCGGCCCAGCACATGGTCCAGTATTTCACAGCCA 1018	839 CAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGGCCAAAGGCAACCGGCTGGTGCTCA 898	424 GGGTGGAAGACGTAATCGCCGAGCTGCGGCTGCGGCAGAGAGCCAAGAGTGGGCA 483 719 ACATGTACGTGCGGGGGTTGTCGGGGGGTGAGCGCAGGAGTCAGCATTGGGGTGCAGC 778 11
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RESULT HSM072C HSM072C ID HS XX AC BX XX XX AC BX XX AC BX XX XX AC BX XX XX AC BX A	Db Db Db	Qy Db Qy	0y 0y	Qy Qy Db	Qy Qy Db	. Db	Qy Db
IT 3 72006 HSM072006 standard; RNA; EST; 691 BP. BX481838; BX481838.1 09-MAY-2003 (Rel. 75, Created) 09-MAY-2003 (Rel. 75, Last updated, Version 1)	U1 00 U1 U2 U2	2399 GATATGCATTTÄTATAGGCAACTCGATATAGGATGGGAGCAAACTAAGGAATGAAT	2279 AGGATGCAGTAGAATAAAGACAGTCGAAAGGGATTTCTGCTCACTGGCAGGAGACTGCG	2159 GCAGACCCTTCAACTGCACTCCCTCCTCAGGAGCACCTTCCTGGGGACAGTGAGGACAAT	2039 TCATTGGCCTCAGCGGTGCTTCATGGTCCTGTACTACGTGTCCTTAAGGTTCAAAC	9 9 9	

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Matches 683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Olagen (Hilden/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (07-MAY-2003) to the MIPS, Ingolstaedter Landstr.1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                               AAATCCTCAGTGCCATGGAGCTGGACTCGTACCCTCTCTACGCCATCTACCTCATCGTCA 2041
                                                                                                                                                                              TCAGCAGAAGAACTTATAAAATGCCTCTCGGGAACCTCACCATCGCGGTCTCAGGAGATA 1981
                                                                                                                                                                                                                           CGTGGATTTCCAAAGTGTCCTTCCTGCGGTGGTGTTTTGAAGGCTGATGAAGATTCAGT 1921
GACCCTTCAACTGCACTCCCTCCTCAGGAGCCCCTTCCTGGGGACAGTGAGGACAATGAC
                      AACCAAGTCAAGACTGGTGATTCACGCCAGACGTCTGCCCGCTGGTGGGGGACCTGAGCA
                                                                   TCAGCAGAAGAACTTATAAAATGCCTCTCGGGAACCTCACCATCGCGGTCTCAGGAGATA
                                                                                                                                                                                                              CGTGGATTTCCAAAGTGTCCTTCCTGCGGTGGTGTTTTGAAGGGCTGATGAAGATTCAGT
                                                                                                                                                                                                                                                              ACTCCTTCTACCTCGCCGGGGGCTTCATGATAAACTTGAGCAGCCTGTGGACAGTGCCCG
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                                              AACCAAGTCAAGACTGGTGATTCACGCCAGACGTCTGCCCGCTGGTGGGGGACCTGAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the German Genome Project.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="DKFZp686M06227"
/clone_lib="686 (synonym: hlcc3). Vector
DH10B; sites SfiIA + SfiIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                        161 A; 200 C; 168 G; 162 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
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TITLE
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                                                                                                                al Similarity
639; Conser
                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM11332 row: a column:
Plate: LLAM11332 row: a column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institutes of Health,
GCTGACTTCTATGTGGACCTGACCAGCATTGACAGGCGCAGCAGCAGAGAGCAGGAATTGGCC
                                                                   CAGCACATGGTCCAGTATTTCACAGCCATCGGCTACCCCTGTCCTCCGCTACAGCAATCCT 1050
                                               ATGCATTTATATAGGCAACTCGATA 2426
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/db_xref="taxon:10000"
/clone="IMAGE:5135115"
/lab_host="PH10B (TI phage-resistant)"
/lab_host="PH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_L19"
/clone="Organ: liver; Vector: pCMV-SPORT6; Site_1
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1
/cloned unidirectionally. Primer: O
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
3. 251 c 203 g 216 t
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/strain="FVB/N"
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Consortium

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                                                                            Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Verte

Mammalla; Eutheria; Rodentia; Sciurognathi; M

1 (bases 1 to 549)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anat
                      Other_ESTs: maa27c08.x1
Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
                                                            Tumor Gene Index Unpublished
                                                                                                                                                                                                BF660076 549 bp mRNA linear EST 20-DEC-2000 maa27ac08.yl NCI_CGAP_Lil0 Mus musculus cDNA clone IMAGE:3812342 5/ similar to TR:Q9VQN4 Q9VQN4 CG9664 PROTEIN. ; mRNA sequence.
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                                                                                                                                                   Mus musculus (house mouse)
  Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies,
                                                                                                                                                                               BF660076.1
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                    GCCTCAGCGGTGGCTTCATGGTCCTGTACCTACGTGTCCTTAAGGTTCATCAAACAGAAAC
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GCATCAGCTACGGCTTCCTGTTCCTGTACTATCCTTGAAGCTCATCAAACAGAAGT
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/lab_host="pH108 (Tl phage-resistant)"
/clone_lib-"NCI_CGAP_Li10"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Library constructed by Life
Technologies."
175 c 110 g 156 t
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/mol_type="mRNA"
/db_xref="taxon:10090"
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King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, I., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, R., Shanada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, I., Yang, I., G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, I., Yang, I., G., Wynshaw-Boris, A., Yanagisawa, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa; I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRL:http://genome.gsc.riken.go.jp/
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishi1,Y., Itoh,M., Kagawa,J., Kawai,J., Kojima,Y., Kondo,S., Konno
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Sasaki,D., Sato,K., Shibata,K., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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BY705076 RIKEN full-length enriched, adult male liver Mus cDNA clone 1300003C16 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
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The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                  yenes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome
10 (11), 1757-1771 (2000)
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/clone_lib="RIKEN full-length enriched, adult male liver"
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/strain="C57BL/6J"
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457 bp mRNA linear EST 22-MAR-1:
IMAGE: 111915 3', mRNA sequence.

N T91380

T91380.1 GI:723293

SEST:
Homo sapiens (human)
ISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

L (bases 1 to 457)

K Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

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Insert Size: 827
High quality sequence stops: 379 Source: IMAGE Consortium, LLNI
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 827 Std Error: 0.00
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Contact: Wilson RK
 TGCGATGACTGGGAGAAAACCTGCACTCGGTGGCNCCCTACAACGTTGCTAATTTATTTC
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//abb_host="PHIOB (ampicillin resistant)"
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/db_xref="taxon:9606"
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/mol_type="mRNA"
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Euteleostomi; Mammalia;
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EMBL/GenBank/DDBJ databases D-85764 Neuherberg, GERMANY В., Amid ი: Osanger Fobo

sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) with sequencing consortium of the German Genome Project. This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Ca Research Center (DKFZ); Email s. Wiemann@dkfz-heidelberg.de; This clone (DKFZp686F02230) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg (Email: clone@rzpd.de within the German Cancer CDNA

/clone_lib="686 (synonym: hlcc3). DH10B; sites SfiIA + SfiIB" /tissue_type="cDNA-collection" Vector pSport1_Sfi; host

Length

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                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Bayashizaki,Y., Cazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
                                                                                                                                                                 encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kou, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasak, D., Shibatta, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
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Arakawa, T., Carninci, P., Fukuda, S.,
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                                                             Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                           Human Genome Sequences. Mamm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-45-503-921
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                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                       Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                       Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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GCCTCAGCTGGTGAGGAAGTGCGTTGCC
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                                                                                                                                                                      GCTGGCCATCATAGGGAGCTCAGGTTGTGGGAGAGCCTCCTTGCTAGATGTGATCACTGG
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127 c 148 g 93 t
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/db_xref="taxon:10090"
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83.7%;
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Pred. No. 2.7e-71;
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511 bp u115h01.yl Sugano mouse embryo m IMAGE:1885393 5', mRNA sequence. AI157365 AI157365.1 l (bases

GI:3685834

mewa

mRNA a Mus

musculus linear

CDNA

EST 30-SEP-1998

WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Contact: Marra M/Mouse EST Project Unpublished The WashU-HHMI Mouse EST Project Mus musculus Mus musculus (house mouse) 1 to 511) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus Louis, **₹**

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T84531 564 bp mRNA linear EST 17-MAR-1995 yd53b02.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                             CTCTCAGGTCCCTTGGTTTGAGCAGCTGGCTCAGTTCAAGATGCCCTGGACATCTCCCAG
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                                                                                                                                                          AGGCAGAGGCCACGGTGGCAAGATGAAATCAGGACAAATTTGGATAAATGGGCAACCCAG
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Site_2: Draili (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a Draili adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct Draili
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' med primer
CTTCTGCTCTAAAAGCTGCG and 3' end primer
CACCTGCACCTCGACCACA."
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/lab_host="DH10B"
/Clone_11b="Sugano mouse embryo mewa"
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/mol_type="mrNA"
/strain="C57BL"
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/clone="IMAGE:1885393"
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Pred. No. 3e-69;
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                                                           2051. GCGGTGGCTTCATGGTCCTGTACTACGTGTCCTTAAGGTTCATCAAACAGAAACCAAGTC
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T84531.1
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                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                      GTGCCATGGAGCTGGACCTCGTACCCTCTACGCCATCTACCTCATCGTCATTGGCCTCA
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98.9%;
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., I Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stops: 383 Source: IMAGE Consortium, LLNL This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 827 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Insert Size: 827
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                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:111915"
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/mol_type="mRNA"
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Score 318.4; DB 14;
Pred. No. 4.4e-68;
0; Mismatches 1;
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                                      Length 564;
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Mus musculus
Mus musculus
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
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WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:969782
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AI151811.1 GI:3680280
                                                                                                                                           Similarity
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CATGGCTGAGAAAACCAAAGAAGAGACCCAGCTGTGGAATGGGACTGTACTTCAGGATGC 119
                                 CATGGCCGGGAAGGCGCCAGAGGAGAGGGCCTGCCCAAAGGGGCCACTCCCCCAGGATAC 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: PMEJBS-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct Dra
sites of the pMEJBS-FL3 vector (5' site CACTGTGTG, 3';
cACCATGTG). XhoI should be used to isolate the cDNA
                                                                                                                                                                                                                                                                           CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                        <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer Common Primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end primer Sequencing: 5' end prim
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/lab_host="DH10B"
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/clone="IMAGE:1885458"
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/strain="C57BL"
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                                                                                                            Score 309.8; DB 9;
Pred. No. 5.7e-66;
0; Mismatches 72;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vj35a03.rl Stratagene mouse diaphragm (#937303) Mus musculus clone IMAGE:930988 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                              Seq primer: -28m13 rev1 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                               quality sequence stop:
Location/Qualifiers
                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="MAGE:930988"
/tissue_type="diaphragm"
/dev_stage="adult"
/clone_lib="Stratagene mouse diaphragm (#937303)"
/note="Organ: diaphragm; Vector: pBluescript SK-;
ECORI; Site_2: XhoI; Cloned unidirectionally from
                                                                           /lab_host="SOLR (kanamycin resistant)"
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    Email: bkoop@uvic.ca
Genome Sciences Centre, BC Cancer Agency cDNA preparation,
sequencing and bioinformatics: Y Butterfield, R Kirkpatrick, J
Asano, N Girn, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prahbu, D
Smailus, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and
                                                                                                                   Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria
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                                                                                         Tel: 250 472 4067 Fax: 250 472 4075
                                                                                                                                                                                                                          GRASP Consortium, Davidson, W.S., Koop, B.F. and http://web.uvic.ca/cbr/grasp.
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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AI597406 398 bp mRN vj33a03.yl Stratagene mouse diaphragm clone IMAGE:930988 5', mRNA sequence. AI597406 I GI:4606454
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1510 TGTTACTCAGAGAGGGCAATGCTTTACTATGAACTGGAAGACGGGCTGTACACCACTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/WashU-NCI Mouse EST Project 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., The WashU-NCI Mouse EST Project 1999
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Mus musculus (house mouse)
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Fax: 314 286 1810
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
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                                     AGCATCCAGCTCTCCTTCATGGATACAGCCGCCCTCTTGTTCATGATCGGTGCTCTCATC 1476
                                                                                                              CATGGGGCGGAGGCCTGTCTGATGTCAATGACCATCGGCTTCCTCTATTTTTGGCCATGGG 1416
                                                                                                                                                                                                                                                                                                                                                         CTGTGGAAAGCTGAGGCAAAGGAACTCAACACAAGCACCCACACAGTCAGCCTGACCCTC
                                                                                    CATGGGTCGGAAGCCTGCCTGATGTCCCTCATCATTGGCTTCCTTTACTACGGCCATGGG
                                                                                                                                                                              TCCACCCTGATCCGTCGGCATTTCCAATGACTTCCGGGACCTGCCCACGCTGCTCATT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="SOLR (kanamycin resistant)" (#937303)" /clone_lib="Stratagene mouse diaphragm (#937303)" /note="Organ: diaphragm; Vector: pBluescript SK:: Site_1: EcoRI; Site_2: XhOI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGAGTTTTTTTTTTTTTTTT 3'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:10090"
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/mol_type="mRNA"
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dev_stage="adult"
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Pred. No. 2.6e-47;
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Search completed: July 27, 2003, 08:29:31 Job time : 4970.41 secs

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Result
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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US-09-866-866A-26
US-09-961-086-2
US-09-981-353-34
US-10-120-687-60
US-09-866-866A-9
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9675:628 Million cell updates/sec
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Sequence 26, Appl
Sequence 2, Appli
Sequence 34, Appl
Sequence 60, Appl
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APPLICANT: Hobbs, Held
APPLICANT: Shan, Bei
                                                                                                                                                                                                                                                                                                                        SEQ ID NO 7
                                                                                                                      Query Match
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Barnes,
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		Sequence 5662, Ap	4059	Sequence 918, App		2	Sequence 1, Appli	Sequence 6449, Ap	Sequence 4811, Ap	Sequence 2722, Ap	Sequence 662, App	Sequence 1, Appli	1	7.	۲,		Sequence 12, Appl	ω.		64	22	5514,	43	Sequence 9, Appli	e 68,	Sequence 196, App		Sequence 12839, A

ALIGNMENTS

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; NAME/KEY: CDS
; LOCATION: (100)..(2121)
OTHER INFORMATION: human ABCG8 (hABCG8)
US-09-989-981A-7
                                                     Best Local Similarity 100 Matches 2669; Conservative
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR EILING DATE: 2000-11-28
NUMBER OF CENTER 11-28
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/252,235 PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/989,981A CURRENT FILING DATE: 2002-07-23
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Board of Regents, The University of Texas System TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methorile REFERENCE: 018781-007320US
                                                                                                                                                                                                           LENGTH: 2669
TYPE: DNA
ORGANISM: Homo sapiens
PatentIn Ver.
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Tularik Inc.
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Pred. No. 0;
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APPLICANT: Tularik Inc.

APPLICANT: Tularik Inc.

APPLICANT: Board of Regents, The University of Texas System
ITILE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of
FILE REFERENCE: 018781-00732009

CURRENT APPLICATION NUMBER: US/09/989,981A

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/252,235

PRIOR APPLICATION NUMBER: US 60/252,645

PRIOR APPLICATION NUMBER: US 60/253,645

PRIOR APPLICATION NUMBER: US 60/253,645

PRIOR APPLICATION NUMBER: US 60/253,645

PRIOR PILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 2019
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IS-6quence 3, Application US/09989981A
Publication US20030049730A1
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                                                                               Query Match
Best Local S
Matches 1659
                                                                                                                FEATURE:
NAME/KEY: CDS
LOCATION: (1). (2019)
OTHER INFORMATION: mouse ABCG8 (mABCG8)
09-989-981A-3
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APPLICANT: Shan, Bei
APPLICANT: Barnes, Robert
APPLICANT: Tian, Hui
                                                                                                                                                                LENGTH: 2019
TYPE: DNA
ORGANISM: Mus musculus
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TCGGGCCTCCAGGATAGATTGTTCTCCTCTGAAAGTGACAACAGCCTGTACTTCACCTAC
                                                 ATGGCCGGGAAGGCGGCAGAGGAGAGGGGCTGCCGAAAGGGGCCACTCCCCAGGATACC
                                      ATGCCTGAGAAAACCAAAGAAGAGACCCAGCTGTGGAATGGGACTGTACTTCAGGATGCT
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APPLICANT: Tian, Hui
APPLICANT: Schultz, Joshua
APPLICANT: Shan, Bei
APPLICANT: Shan, Bei
APPLICANT: Shan, Bei
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG):
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION.NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                         GENERAL INFORMATION:
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Patent No. US20020081687A1
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; LCCATION: (107)...(2062)
; OTHER INFORMATION: human sitosterolemia
; OTHER INFORMATION: protein
US-09-837-992-4
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Best Local Sim
Matches 432;
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PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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ilarity 54.4%;
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 5
LENGTH: 2340
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (107)..(2062)
; OTHER INFORMATION: human ABCGS (hABCGS)
US-09-989-981A-5
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Best Local (
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CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/253,645 PRIOR FILING DATE: 2000-11-28
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APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTIO: ABCG5 and ABCG8: Compositions and Methor
FILE REFERENCE: 018781-007320US
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      CCACCTCTGGGCTCGACAGCTTCACAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGG
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                                                              GCCGGGTCTCCATCGCAGCCCAGCTGCTCCAGGATCCTAAGGTCATGCTGTTTGATGAGC
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Pred. No. 1.2e-50;
0; Mismatches 359;
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, NAME/KEY: CDS
; LOCATION: (1)..(1959)
; OTHER INFORMATION: mouse ABCG5 (mABCG5)
US-09-989-981A-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      Matches 429;
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APPLICANT: Tularik Inc.
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Method
FILE REFERENCE: 018781-007320US
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APPLICANT: Shan, Bei
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                                      GCTCGCCTCAGCTGGTGAGGAAGTGTGTGGCCCACGTGCGCCAGCAACCAGCTGCTCC
                                                                         CCGGGAGGCTGCGGCGCACTGGGACCCTGGAAGGGGAGGTGTTTGTGAATGGCTGCGAGC 361
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                                                                                                                                                      SEQ ID NO 2
                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                     APPLICANT: Shan, Bei
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG):
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT FILING DATE: 2001-04-18
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tian,
FEATURE: OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG) NAME/KBY: CDS LOCATION: (47)..(2005) COTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG) OTHER INFORMATION: protein
                                                                                                                           TYPE: DNA
                                                                                                      ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                     Schultz, Joshua
                                                                                                                                                                                                                                                                                                                      Compositions
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RESULT 7

US-09-866-866A-13

Sequence 13, Application US/09866866A

; Patent No. US20020102244A1

; GENERAL INFORMATION:
   APPLICANT: Sorrentino, Brian
   APPLICANT: Schuetz, John
   TITLE OF INVENTION: A Method of Identifying and
   FILE REFERENCE: 1340-1-021CIP2
   CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
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Conservative
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Pred. No. 1.5e-47;
0; Mismatches 371;
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Length

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Gaps

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607

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667

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US-09-866-866A-26
; Sequence 26, Application US/09866866A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Mus
US-09-866-866A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 278; Conserv
                                                                                                             APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
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                                                                         PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                        APPLICANT: Sorrentino, Brian APPLICANT: Schuetz, John
                                                      PRIOR APPLICATION NUMBER: 60/086,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGGTTACCACTGTGAGCCCTACAACAACCCTGCGGATTTTTTCCTTGATGTCATCA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGCCTACCCCTCTCCTCCCTACAGCAATCCTGCTGACCTTCTATCTGGACCTGACCA 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTTCCGGGAAACTCGTGTTCCATGGGCCAGCACAGAAGGCCTTGGAGTACTTTGCATCA 853
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                                  DATE: 1998-05-28
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Pred. No. 5.8e-26;
0; Mismatches 260;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-961-086-2
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                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09961086 Publication No. US20030036645A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 26 LENGTH: 2247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 269;
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Best Local :
                                                                                                                                                                                                                                                                                    APPLICANT: ABRUZZO, Lynne
TITLE OF INVENTION: BREAST CANCER RESISTANCE PROTEIN (BCRP) AND THE DNA
TITLE OF INVENTION: WHICH ENCODES IT
FILE REFERENCE: EP19376-019
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: UNIVERSITY OF MARYLAND, BALTIMORE APPLICANT: ROSS, Douglas D. APPLICANT: DOYLE, L. Austin
                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/073,763
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: PCT/US99/02577
PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/961,086 CURRENT FILING DATE: 2001-09-21
                                                                                                           SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                    LENGTH:
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ORGANISM: Homo
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Pred. No. 6e-2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/09981353 Patent No. US20020160382A1 GENERAL INFORMATION:
                                                                                                     Query Match 4.3%;
Best Local Similarity 51.2%;
                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                             APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT APPLILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
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Best Local Similarity
Matches 269; Conserv
                                                                                                                                                                                                                                                                 SOFTWARE: PERL Program
                                                                                                                                                                                                      LENGTH: 2574
TYPE: DNA
ORGANISM: Homo saplens
                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020160382A1 5517972CB1
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                      ID NO 34
ENGTH: 2574
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                            ACGTGGTACAAGATGATGTGGTGATGGGCACTCTGACGGTGAGAGAAAACTTACAGTTCT
                                                        ACGTGCGCCAGCACCAGCTGCTCCCCAACTTGACTGTGCGAGAGACCTTGGCCTTCA
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                                                                                      Score 115.4; DB 1
Pred. No. 6.5e-24;
0; Mismatches 256
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Pred. No. 6.3e-24;
0; Mismatches 256;
                                                                                                                 DB 10;
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; TYPE: DNA
; ORGANISM: Homo
US-10-120-687-60
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US-10-120-687-60
                                                                                                                                                                                              Matches
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Best Local Similarity
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SEQ ID NO 60
LENGTH: 2718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/963,879
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/215109
PRIOR APPLICATION NUMBER: US 60/238880
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/120,687
CURRENT FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Massachusetts General Hospital TITLE OF INVENTION: Stem Cells of the Isl TITLE OF INVENTION: Mellitus FILE REFERENCE: 3284/1235B
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/731261 PRIOR FILING DATE: 2000-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US60/169082
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                                          TTGCCCAGATGCGGCTGCCCAGAACCTTCTCCCAGGCCCAGCGTGACAAAAGGGTGGAGG 667
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                                                                                           ACGTGGTACAAGATGATGTTGTGATGGGCACTCTGACGGTGAGAGAAAACTTACAGTTCT
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llarity 51.2%;
Conservative
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Pred. No. 6.6e-
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Best Local Similarity 51.2%;
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                                                                                                                                                                                                                                                                                                                                        Matches
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TITLE OF INVENTION: A method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR PILING DATE: 2000-05-31
PRIOR PILING DATE: 2000-05-31
PRIOR FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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TYPE: DNA
ORGANISM: Homo sapiens
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                                               TGCGGGGGTTGTCGGGGGGTGAGCGCAGGAGAGTCAGCATTGGGGTTGCAGCTCCTGTGGA 787
                                                                                                                               ACGTGATCGCGGAGCTGCGGCTTAGGCAGTGCGCTGACACCCGCGTGGGCAACATGTACG 727
          TCCGTGGTGTGTCTGGAGGAGAAAGAAAAAGGACTAGTATAGGAATGGAGCTTATCACTG 811
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Pred. No. 6.6e-24;
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: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-072-621-5
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LENGTH: 3201
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APPLICANT: Pollard, Michelle
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR I
FILE REFERENCE: 100103.402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/072,621 CURRENT FILING DATE: 2002-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 4.0%;
Local Similarity 44.4%;
nes 683; Conservative
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TCGGGGGGTGAGCGCAGGAGACTCAGCATTGGGGTGCAGCTCCTGTGGAACCCCAGGAATC 798
                                                                                                  GAGCTGCGGCTTAGGCAGTGCGCTGACACCCCGCGTGGGCAACATGTACGTGCGGGGGTTG 738
                                                                                                                                           AAGCTTCAGGAGAAGG-----ATGAAGGCAGAAGGGAAATGGTCAAGGAGATACTGACA 863
                                                                                                                                                                                                                       GATGACATGCTGCCGCATCTCACTGTGCAGGAGGCCATGATGGTGTCGGCACATCTG
                                                                                                                                                                                                                                                              CACAACCAGCTGCTCCCCAACTTGACTGTGCGAGAGACCTTGGCCTTCATTGCCCAGATG
                                                               CCTGTCCTCGCTACAGCAATCCTGCTGACTTCTATGTGGACCTGA 1072
                                                                                                                                                                                CGGCTGCCCAGAACCTTCTCCCAGGCCCAGCGTGACAAAAGGGTGGAGGACGTGATCGCG
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CTCGCCGGGGCTTCATGATAAACTTGAGCAGCCTGTGGACAGTGCCCGCGTGGATTTCC
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                                                                                                                                                                                                                                                  TGCAGCATCGTGTACTGGATGACGTCGCAGCCGTCGGACGCCGTGGCCTTTGTGCTGTTT
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Best Local Similarity 44.3%;
Matches 682; Conservative
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LENGTH: 2930
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PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0
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CCURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/298,914
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 366
SEQ ID NO 276
LENGTH: 2930
TYPE: DNA
ORGANISM: HOMO SAPIENS
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-276
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Best Local Similarity 44.3%;
Matches 682; Conservative
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APPLICANT: Linsley, Pe
APPLICANT: Mao Mao
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APPLICANT: Mao Mao
TITLE OF INVENTION: Signature Genes in
FILE REFERENCE: 9301-157-999
                                  1039 TACAGCAATCCTGCTGACTTCTATGTGGACCT---GACCAGCATTGACAGGCGCAGCAGA
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TACCACAACCCAGCAGATTTTGTCATGGAGGTTGCATCCGGCGAGTACGGTGATCAGAAC
                                                                        CGGGGAAAAGTCTGCAATCTTGTGCCATATTTGAGGGATTTGGGTCTGAACTGCCCAACC
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                                                                                          CTGTTCTCGGGGTTCTTCGTCAGCTTCGACACCATCCCCACGTACCTACAGTGGATGTCC 1809
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Search completed: July 27, 2003, 08:56:18 Job time: 583.074 secs

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Post-processing: Minimum Match 0%
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Sequence 11600, A
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sequence 2, Appli Sequence 6149, Ap		5054,	Sequence 5014, Ap Sequence 5107, Ap	5139,								8469	24,	Sequence 22, Appl

GENERAL INFORMATION:

APPLICANT: Doyle, L. Austin

APPLICANT: Abruzzo, Lynne V.

APPLICANT: Ross, Douglas D.

TITLE OF INVENTION: Breast Cancer Resistance Proceedings of the Conversion of the SEQ ID NO 2 ; LENGTH: 2418 ; TYPE: DNA ; ORGANISM: Human MCF-7/AdrVp cells US-09-245-808-2 906 CTGTCCTTTTGCTCCTGAAAAGGATGTCTAAGCAGGGACGAACAATCATCTTCTCCATTC 726 GGGTCATTCAAGAGTTAGGTCTGGATAAAGTGGCAGACTCCAAGGTTGGAACTCAGTTTA 668 ACGTGATCGCGGAGCTGCGGCTTAGGCAGTGCGCTGACACCCGCGTGGGCAACATGTACG 608 TTGCCCAGATGCGGCTGCCCAGAACCTTCTCCCAGGCCCCAGCGTGACAAAAAGGGTGGAGG 667 606 ACGTGGTACAAGATGATGTTGTGATGGGCACTCTGACGGTGAGAGAAAACTTACAGTTCT 665 ATCCTTCCATCTTGTTCTTGGATGAGCCTACAACTGGCTTAGACTCAAGCACAGCAAATG ACCCAGGAATCCTTATTCTCGACGAACCCACCTCTGGGCTCGACAGCTTCACAGCCCACA 847 TGCGGGGGTTGTCGGGGGGTGAGCGCAGGAGAGTCAGCATTGGGGTGCAGCTCCTGTGGA 787 Application US/09245808 4.3%; 51.2%; Score 115.4; DB 4 Pred. No. 6.3e-19; 0; Mismatches 256 ALIGNMENTS DB 4; 256; Protein (BCRP) and DNA which Indels Length 2418; 0 Gaps 907 845 965 727 725

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PRIOR FILING DATE: 1998-07-27 
NUMBER OF SEQ ID NOS: 33142 
SEQ ID NO 14568 
LENGTH: 747
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING
TOP INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TOP DIAGNOSTICS AND THERAPEUTICS
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Best Local Similarity
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 CAGCTTCACAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGGCCAAAGGCAACCGGCT 890
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Pred. No. 7:7e-06;
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: Sequence 14337, Application US/09252991A

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Best Local Similarity
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PRIOR ETLING DATE: 1998-UZ-1V
PRIOR APPLICATION NUMBER: US (
PRIOR APPLICATION DATE: 1998-07-27
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                                                                                      CAGCTTCACAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGGCCAAAAGGCAAACCGGCT
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 7.8e-06;
0; Mismatches 274;
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GENERAL INFORMATION:

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US-09-252-991A-14279
Sequence 14279, Application US/09252991A
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14340
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; Patent No. 6551795
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Best Local Similarity
Matches 273; Conserv
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14340
LENGTH: 1311
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TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Pred. No. 9.4e-06;
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Best Local Similarity
Matches 273; Conserv
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LENGTH: 1374
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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1215 CATGGTCCTGGTCACCCACGAGATCCGCTTCGCC 1248
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                                                                                             CAGCTTCACAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGGCCAAAGGCAACCGGCT
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Pred. No. 9.6e-06;
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PALELL
GENERAL INFURE...
APPLICANT: Tang, Y. 10...
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
Ren, Feiyan

RESULT 6 US-09-620-312D-918

Sequence 918, Application US/09620312D Patent No. 6569662

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SOFTWARE: pt_FL_genes
SEQ ID NO 918
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
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LOCATION: (1)
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TTLE OF INVENTION: No. 6569662el Nucleic Acids and ITLE OF INVENTION: Polypeptides
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Wang, Zhiwei
John Tillinghast
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Yang, Yonghong
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US-08-232-463-14
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FONLPOX VIRUS
                                                                                                                                                                                                                          IMMEDIATE SOURCE:
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MEDIUM TYPE: Floppy disk
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TELEFAX: 899149
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APPLICATION NUMBER:
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TOPOLOGY: lir
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                       (703)683-4109
                                                                                                                          2.0%; Score 54.6; DB 1 larity 3.8%; Pred. No. 0.00093; Conservative 221; Mismatches 15
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Best Local Similarity
Matches 187; Conserv
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CURRENT FILING DATE: 1998-06-24
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SOFTWARE: Patentin Ver.
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OTHER INFORMATION:
OTHER INFORMATION:
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                        GENERAL INFORMATION:
APPLICANT: MATC J. FITTLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 1071
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                                                                                                                                                         Sequence 11541, Application US/09252991A Patent No. 6551795
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  CURRENT APPLICATION
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; ORGANISM: Mycobacterium tuberculosis; OTHER INFORMATION: H37Rv US-09-103-840A-I
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nes 187; Conserv
GGTGGTGCTCGTGGTTACCCAC 1975160
                                              GCTGGTGCTCATCTCCCTCCAC 909
                                                                                                                                             CGACAGCTTCACAGCCCACAACCTGGTGAAGACCTTGTCCAGGCTGGCCAAAGGCAACCG
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Pred. No. 0.013;
0; Mismatches 180;
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Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMO AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER:

US/09/252,991A

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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-11845
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                                                                                          SEQ ID NO 11845
LENGTH: 1155
TYPE: DNA
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 11845, Application US/09252991A Patent No. 6551795
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Best Local
                                                                                                                                                           PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                         APPLICANT: MATE J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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-09-252-991A-11541
                                                                                                                                                NUMBER OF SEQ ID NOS:
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11541
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Pred. No. 0.0025;
0; Mismatches 246; Indels
51.4; DB 4
               4;
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LENGTH: 2367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11600, Approximately Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMON;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Local Similarity 46.0%;
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GCCGGAGAACGTGACCTTCTACCCGCAGCTCAGCGGCGCGGGAAACCCCTGCGCCACTTCGC
                                GCGACAGACCTTGGCCTTCATTGCCCAGATGCGGCTGCCCAGAACCTTCTCCCAGGCCCA 647
                                                                      CGTGCGGGTCCTCGGCCACGATGCGAGGAGGCCTGGAGGCGGCGGCCAGCTCGGCTACCT
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Pred. No. 0.0038;
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                                                                 Query Match
                             Best Local Similarity
Matches 148; Conserv
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                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                   MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/377,440

FILING DATE: 24-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: COLUMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: MIKOLAJCZAK, MARCIA
PPLICANT: ARMENTROUT, RICHARD W.
ITLE OF INVENTION: DNA SEGMENTS AND METHODS FOR INCREASING
                                                                                                                                                      TOPOLOGY: unknown
                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                 NAME: GOLDBERG, JULES REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10016-2391
                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: JULES E.
                                                                                                                                                                                                        ENGTH:
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                        Score 51.4; DB 2;
Pred. No. 0.0094;
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APPLICANT: Armentrout, Richard W
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 28804
TYPE: DNA
ORGANISM: Sphingomonas sp. S88
US-09-096-867-2
Search completed: July 27, 2003, 12:45:54 Job time: 182.378 secs
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Best Local Similarity 47.9%;
Matches 148; Conservative
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EARLIER APPLICATION NUMBER: 60/049,428
EARLIER FILING DATE: 1997-06-12
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TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris
FILE REFERENCE: seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096,867
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APPLICANT: Mikolajczak, Marcia
APPLICANT: Yamazaki, Motohide
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Pred. No. 0.0094;
0; Mismatches 161; Indels 0;
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OM protein - protein search, using sw model
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: June 11, 2003, 09:04:42; Search time 15 Seconds (without alignments).
1800.073 Million cell updates/sec

Title: Perfect score: US-09-989-981A-6 3326

Sequence: MGDLSSLTPGGSMGLQVNRG......PALVILGIVVFKIRDHLISR 651

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Patel S.B.;

"Two genes that map to the STSL locus cause sitosterolemia: genomic structure and spectrum of mutations involving sterolin-1 and sterolin-2, encoded by ABGC5 and ABCG8, respectively.";

Am. J. Hum. Genet. 69:278-290(2001).

-i- FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the

liver into bile. SUBUNIT: May for

form heterodimers with ABCG8 or be tightly coupled to

MEDLINE-21344600; PubMed-11452359;
Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H., Kojima H.,
Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H., Kojima H.,
Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H., Kojima H.,
Pandya A., Brewer H.B. Jr., Salen G., Dean M., Srivastava A.K.,

VARIANTS SITOSTEROLEMIA Q-146; H-389; P-419; H-419 AND S-550, AND VARIANT E-604

ALIGNMENTS

RESULT	TCT 1
ABG5	LHUMAN
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SO	Homo sapiens (Human).
8	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
8	Primates: Catarrhini: Hominidae:
o x	
RN	[1]
RP	SEQUENCE FROM N.A., AND VARIANT GLU-604.
RC	iver;
æ×	MEDLINE=20553648; PubMed=11099417;
RA	Berge K.E., Tian H., Graf G.A., Yu L., Grishin N.V., Schultz J.,
▼ RA	
RT	"Accumulation of dietary cholesterol in sitosterolemia caused by
RT	ansporters.";
RL	Science 290:1771-1775(2000).
RN	[2]
RP	SEQUENCE FROM N.A., VARIANTS SITOSTEROLEMIA H-389; H-419 AND P-419,
RP	
RC	TISSUE=Liver;
RX	753;
RA	Lee MH., Lu K., Hazard S., Yu H., Shulenin S., Hidaka H., Kotima H.,
RA	Pegoraro R., Srivastava A.K., Salen G.,
RA	l S.B.;
RT	"Identification of a gene, ABCG5, important in the regulation of
RT	lesterol absorption.";
RL	Nat. Genet. 27:79-83(2001).
RN	[3]
RP	REVIEW.
ЯX	MEDLINE=21474438; PubMed=11590207;
RA	Schmitz G., Langmann T., Heimerl S.:
RT	ABCG family members in limid metabolism *
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RN	[4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD00000
SMART; SM00382;
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                                                                                                                                                                                                         VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:13886; ABCG5
MIM; 605459; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             absorption of all sterols including cholesterol, plant and shellfish sterols, and decreased biliary excretion of dietary sterols into bile. Sitosterolemia patients have hypercholesterolemia, very high levels of plant sterols in the plasma, and frequently develop tendon and tuberous xanthomas, accelerated atherosclerosis and premature coronary artery disease. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: Defects in ABCG5 are a cause of sitosterolemia, also known as phytosterolemia or shellfish sterolemia, a rare autosomal recessive disorder characterized by increased intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        excretion.
SUBCELLULAR LOCATION: Integra
TISSUE SPECIFICITY: Strongly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the small intestine and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABCG8 along a
                        651;
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       M00382; AAA; 1.
PS00211; ABC_TRANSPORTER; FALSE_NEG.
MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSC
                                                                   651 AA;
                      100.0%; ilarity 100.0%; conservative
                                                                                                                                                                                                                                        384
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643
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86
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                                                                                                                                                                                                                 584
591
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ABC_transportr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathway regulating diatery-sterol absorption and
                                                                                          604
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                                                                                                                                    419
                                                                                                                                                           419
                                                                                                                                                                                 389
                                                                  72503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integral membrane
                                                                                                                                                                                                                                                                                                                              2 (POTENTIAL).
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Transport; Polymorphism,
                       0;
                                                                                                                                                                                                 ATP (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

E -> Q (IN SITOSTEROLEMIA).
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5 (POTENTIAL
                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL) 6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL)
                                                                                                                                                                             /FTId=VAR_012244.
R -> H (IN SITOSTEROLEMIA)
                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                 Score 3326;
Pred. No. 1
                                                                  /FTId=VAR_012249.
950BABFCBB6A1536
                                                                                                   /FTId=VAR_012248
                                                                                                             /FTId-VAR_012247.
R -> S (IN SITOSTEROLEMIA)
                                                                                                                                               /FTId=VAR_012246
                                                                                                                                                                     /FTId-VAR_012245
                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
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                                                      dietary cholesterol absorption.";
Nat. Genet. 27:79-83(2001).
[2]
                                                                                                                                                                                                                                                                       ABG5_MOUSE
Q99PE8;
           TISSUE SPECIFICITY, AND INDUCTION.
MEDILINE-2053648; PubMed-11099417;
Berge K.E., Tian H., Graf G.A., YU
Berge K.E., Tian B., Barnes R.,
Kwiterovich P., Shan B., Barnes R.,
                                                                                MEDLINE-20578753; PubMed-11138003; Lee M.H., Lu K., Hazard S., Yu H., Alliknets R., Sakuma N., Pegoraro R. Dean M., Patel S.B.; "Identification of a gene, ABCG5, in dietary characters"
                                                                                                                              STRAIN=C57BL/6; TISSUE-Liver; MEDLINE-20578753; PubMed-1113
                                                                                                                                                                                                                                        15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                         NCBI_TaxID=10090;
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2 (Rel. 41, Last anno
g cassette, sub-famil
    of dietary
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
sub-family G, member
f G.A., Yu L., Grishin N.V., Schultz J
Barnes R., Hobbs H.H.;
cholesterol in sitosterolemia caused
                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                         ₽.
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                    Schultz J.,
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Salen
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n G.,
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutations in adjacent ABC transporters.", Science 290:1771-1775(2000).
                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver into bile.

SUBUNIT: May form heterodimers with ABCG8 ABCG8 along a pathway regulating diatery-s excretion (By similarity).

SUBCELULAR LOCATION: Integral membrane processed specificity: Expressed in the intestivel, in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: Upregulated by cholesterol feeding. Poss by the liver X receptor/retinoic X receptor (LXR/R) SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by the liver x recepsions:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
    181
                         180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF312713; AAG53097.1; -.
                                                                                                                                                                                               Similarity
                                                                                      PD000006;
LRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSH
                                                                                                                                               MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEP-HSLGILHASYSVSHRVRPWWDITS
                                            LRRDQFQDCFSYVLQSDVFLSSLTVRETLRYTAMLALCRSSADFYNKKVEAVMTELSLSH
                                                                                                                                     MGELPFLSPEGARGPHINRGSLSSLEQGSVTGTEARHSLGVLHVSYSVSNRVGPWWNIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00211;
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422
443
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80.1%;
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EXTRACELLULAR (POTENTIAL).

2 (POTENTIAL).

3 (POTENTIAL).

3 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

4 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

5 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
CYTOPLASMIC
                                                                                                                                                                                  Score 2738.5;
Pred. No. 1.3e
64; Mismatches
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                                                                                                                                                                                            5; DB 1;
..3e-183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein (Probable).
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X MEDLINE-20578753; PubMed-11138003;

X Lee M.-H., Lu K., Hazard S., Yu H., Shulenin S., Hidaka H., Kojima H.,

X Allikmets R., Sakuma N., Pegoraro R., Srivastava A.K., Salen G.,

Y Talentification of a gene, ABCG5, important in the regulation of dietary cholesterol absorption.*;

Y Talentification of a gene, ABCG5, important in the regulation of dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion by the confidence of the enterocytes and in the selective sterol excretion in an action of the enterocytes and in the selective sterol excretion of the enterocytes and in the selective sterol excretion of the enterocytes and in the selective ster
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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TRANSPORTER FAMILY. ABCG (WHITE)
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license agreement (See http://www.isb-sib.ch/announce/license@isb-sib.ch).

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                                          VIFSSYCYWTLGLYPEVARFGYFSAALLAPHLIGEFLTLYLLGMYQNPNIVNSIVALLSI
                                                                                                                 VGLLYQFYGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSYVAT
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N-LINKED (GLCNAC. . ) (POTENTIAL).
MW; 4D42FE2BABODAD59 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 2727.5;
Pred. No. 7.7
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4 (POTENTIAL).
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3 (POTENTIA
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2 (POTENTIAL).
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A AIZAWA K., IZAWA M., NIShi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., IZAWA M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., IZAWA M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kachi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Casavant T., Washio T.,
A Kuchi P., Carini I., Mashio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G. T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Worshow P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
A Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Hayashi-Araki Y., Storch K., Sakamoto N.,
A Hayashi-Araki Y., Storch M., Sakamoto N.,
A Hayashi-Araki Y., Storch M.,
A Hayashi-Araki Y., Storch M.,
A Hayashi-Arak
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15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure and spectrum of mutations involving sterolin-
sterolin-2, encoded by ABCG5 and ABCG8, respectively.",
Am. J. Hum. Genet. 69:278-290(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
"Functional annotation of
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY, AND INDUCTION. MEDLINE=20553648; PubMed=11099417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1)
STRAIN=C57BL/6J; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H., Ose L., Stalenhoef A.F.H., Mietinnen T., Bjorkhem I., Bruc Pandya A., Brewer H.B. Jr., Salen G., Dean M., Srivastava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6; T1
MEDLINE=21344600;
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Mammalia; Eutheria; Rodentia;
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level, in the liver.

INDUCTION: Upregulated by cholesterol feeding. Possibly mediated INDUCTION: Upregulated by cholesterol feeding. Possibly mediated by the liver X receptor/retinoide X receptor (LXR/RXR) pathway. by the liver X receptor/retinoide X receptor (LXR/RXR) pathway. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
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(Rel. 41,
(Rel. 41,
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Last annotation update)
sub-family G, member 8
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Sciurognathi; Muridae;
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Bruckert
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amanaka I.,
Saito R.,
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VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000006; ABC_transportr; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
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InterPro; IPR003439; ABC_transportr.
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Similarity
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                                                                 CLMSLIIGFLYYGHGAKQL--
                                                                                                 LIMGLFLLFFYLRVRSNYLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPYLRAVSDQES
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BAB23630.1;
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4 (POTEM.

5 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTEMTIAL).

"TSSING (IN ISOFORM 2).
                                                                                                                                            ·TQDTDCGTAVELPGMIEQFSTLIRRQISNDFRDLPTLLIHGSEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 698; DB
Pred. No. 3.2e-
33; Mismatches
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3 (POTENTIAL)
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2 (POTENTIAL).
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                                                           SFMDTAALLFMIGALIPFNVILDVVSKCHSERSMLYYEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2e-41;
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RESULT 5
ABG8_HUMAN
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    Schmitz G., Langmann T., Heimerl S.;
    Role of ABCG1 and other ABCG family members in lipid metabolism.";
    J. Lipid Res. 42:1513-1520(2001)
    -I- FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the entercoytes and in the selective sterol excretion by the liver into bile.

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                                                                                                                                                                                                                                                                                                                          "Two genes that map to the STSL locus cause sitosterolemia: structure and spectrum of mutations involving sterolin-1 and sterolin-2, encoded by ABCG5 and ABCG8, respectively."; Am. J. Hum. Genet. 69:278-290(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20553648; PubMed=11099417; Berge K.E., Tian H., Graf G.A., Yu L., Gri Kwiterovich P., Shan B., Barnes R., Hobbs "Accumulation of dietary cholesterol in st mutations in adjacent ABC transporters."; Science 290:1771-1775(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002
15-JUN-2002
15-JUN-2002
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Q9H221;
                                                                                                                                                                                                                                                                                                                                                                                                                          Ose L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), VARIANTS SITOSTEROLEMIA H-184; T-231; Q-263; H-405; P-501; S-543; P-572; E-574; R-574; R-596 AND F-570 DEL, AND VARIANTS H-19; C-54; K-238; V-259; K-400; R-575 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                 MEDLINE=21474438; PubMed=11590207;
                                                                                                                                                                                                                                                                                                                                                                                            Patel S.B.;
                                                                                                                                                                                                                                                                                                                                                                                                             Pandya
                                                                                                                                                                                                                                                                                                                                                                                                                                        Lu K., Lee M.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., VARI
R-596, AND VARIANT C-54
                                                                                                                                                                                                                                                                                                 REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21344600; PubMed=11452359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding
                        excretion.
SUBCELL/LIAR LOCATION: Integral membrane protein (Probab ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; produced by alternative splicing. Isoform 2 is a minor detected in approximately 10% of the cDNA clones TISSUE SPECIFICITY: Strongly expressed in the liver, loin the small intestine and colon. Detectable in a wide
                                                                                                                                SUBUNIT: May form heterodimers with ABCG5 or be ABCG5 along a pathway regulating diatery-sterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625
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                                                                                                                                                                                                                                                                                                                                                                                                         A., Brewer H.B. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                        Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H.,
Stalenhoef A.F.H., Mietinnen T., Bjorkhem I., Bru
A., Brewer H.B. Jr., Salen G., Dean M., Srivastava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPLYAIY --LIVIGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLRWCFSGLMQIQFNGHLYTTQIGNFTFSILGDTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQKYCSEILVVNEFYGLNFT--CGSSNVSVTTNPMCAFTQGIQFIEKTCPGATSRFTMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWLVVFCCRTMALAASAMLPTFHMSSFFCNALYNSFYLTAGFMINLDNLWIVPAWISKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFL----TLVLLGIVQNPNI-VNSYVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFT
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(Rel. 41,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Last sequence update) (Rel. 41, Last annotation updat cassette, sub-family G, member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITOSTEROLEMIA T-231; Q-263; R-574 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nember 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grishin N.V.,
obs H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sitosterolemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Sterolin-2)
                                                                                                                                   be tightly coupled rol absorption and
                                                                                                                                                                                                                indispensable role
                                                                                   (Probable).
) and 2; are
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                                                                                                                                                                                                                                                                                                                                                                                                                     H., Kojima H
Bruckert E.,
                        lower levels
de variety of
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by the
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DISEASE: human tissues

Defects

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ABCG8 are

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cause

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sitosterolemia,

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CARBOHYD
VARSPLIC
VARIANT
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MIM; 210250;
             VARIANT
                                 VARIANT
                                                       VARIANI
                                                                             VARIANT
                                                                                                   VARIANT
                                                                                                                        VARIANT
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DOMAIN
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:13887;
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF351822; AAK84663.1; EMBL; AF351823; AAK84663.1;
                                                                                                                                                                              MAIN
                                                                                                                                                                                                                                                 MAIN
                                                                                                                                                                                                                                                                   NIAMOC
                                                                                                                                                                                                                                                                                                               Polymorphism;
DOMAIN
                                                                                                                                                                                                                                                                                                                                      slycoprotein;
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO
Pfam; PF00005;
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                                                                                                                                                                                                                                                                                                                                                ROSITE;
                                                                                                                                                                                                                                                                                                                                                            roDom; PD000006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                known as phytosterolemia or shellfish sterolemia, a rare autosomal recessive disorder characterized by increased intestinal absorption of all sterols including cholesterol, plant and shellfish sterols, and decreased biliary excretion of dietary sterols into bile. Sitosterolemia patients have hypercholesterolemia, very high levels of plant sterols in the plasma, and frequently develop tendon and tuberous xanthomas, accelerated atherosclerosis and premature coronary artery disease. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAUTION: Seems to have a defective ATP-binding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF351818; AAK84663
AF351819; AAK84663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF351824; AAK84663
                                                                                                                                                                                                                                                                                                                                                PS00211;
                                                                                                                                                                                                                                                                                                                                                                              IPR003439; ABC_transportr.
                                                       238
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                                                                                                   184
                                                                                                                                                                            640
661
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532
553
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417
438
448
469
493
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                                                                                                                                                                                                                                                                                                                          Disease mutation
                                                                                                                                                                                                                                                                                                                                      Transmembrane;
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                                                                                                                                                                                                                                                                                                                                               ABC_transportr; 1.
ABC_TRANSPORTER; 1.
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CYTOPLASMIC (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  Transport; Alternative splicing;
                                                                                                                                                     N-LINKED (GLCNAC. . .)
MISSING (IN ISOFORM 2).
/FTId=VAR_012255.
R -> Q (IN SITOSTEROLEMIA).
/FTId=VAR_012256.
                                                                         /FTId-VAR_012251.
R -> H (IN SITOSTEROLEMIA).
/FTId-VAR_012252.
P -> T (IN SITOSTEROLEMIA).
                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                               /FTId-VAR_012250.
                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
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                                          FTId=VAR_012254.
                                                                FTId=VAR_012253.
                                                                                                                                             V
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550	536	500	447	422	391	363	349	_	295	255	195	175	135	116	76	65	16	8	Query Match Best Local S Matches 187	SEQUENCÉ	VARIANT	VARIANT	VARIANT	VARIANT	VARIANT	VARIANT	VARIANT	VARIANT	VARIANT	VARIANT	VARIANT
RNIQEMPIPFKII	WLVVFCCRI		AVSDQESQDGLYQKW : : AMLYYELEDGLYTTG	: : : AEACLMSMT	LQNLIMGLE	AETKDLDED		SNPADFYVD	SNPFDFYMD	LYELAKKNK : LSRLAKGNR	LRLRQCADT	LSLSHVADR	NGQPSSPQL	RAL	TSPSCQNSC	TRQI	TPQDTSGLQ	PG	imilarit ; Conse	673 AA;	632	596	575	574	574	572	570	543	501	405	400
FKIISYFTFQKYCS	RIMALAAAALEPTEHMASEE	-GYFSAALLAPHL	GLYTTGPYFF.	: IGFLYFG	NLIMGLELLEFYLRYRSNYLKGAIQ	; TKDLDEDTCVESSVTPLDTNC	KTLPM	: : : LTSIDRRSRI	LTSVDTOSKI	TALISTHON	RVGNMYVRG	LIGNYSLGG	VRKCVAHVR	RALRREQFODCFSYVLOS	SPSCQNSCELGIQNLSFKVRSGQMLA	LKDVSL	DRLFSSESD	GSMGLQVNRGSQSSL	21.0%; 28.9%; vative 1	75678 MW	632	596	575	574	574	572	570	543	501	405	400
QKYCSEILVVNEFYGLNFTCGSSNVSVTTN 597	PTFHMASFESGFM	TLVLLGIVQNPNIVNSVVALLSIAGVLVGSG	AVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARF	:	SNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLR	: : : : LPSPTK-MPGAVQQFTTLIRRQISNDFRDLPTLLI	MVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRL	: : ::: LFLEKVRDLDDFLW	YXXXATOHXTIXXITEXXXII	LVELEKKNK. VVLTIHUPKSELEQLEUK LALLSEGELIEGGTPARKLDFENDGGYPCDER 	WNPGILILDEPTSGLDSFTAHNLV	SLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVL	SPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAE	DTLLSSLTVRETLHYTALLAI-RRGNPGSFQKKVEAVMA	: : : :: :: IIGSSGCGRASLLDVITGR-GHGGKIKSGQI	LKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTF-LGEVYV	SGQPNTLEVRDLNYQVDLASQVPWFEQ	SLEGAPAT-APEPHSLGILHASYSVSHRVR-PWWD-ITSCROOW	Score 697; DB 1; Length 673; Pred. No. 3.8e-41; 24; Mismatches 241; Indels 96; Gaps	/FIIG=VAR_01226/. W; 594AFD1D6C1BB50F CRC64;	V -> A. (2000)	L -> R (IN STEROLEMIA).	/FILG=VAR_U12264.	E A	/FIG=VAR_012252. G -> E (IN SITOSTEROLEMIA).	/FIIG=VAR_U12261. L -> P (IN SITOSTEROLEMIA).	MISSING (IN SITOSTEROLEMIA).	/FIG=VAR_012259. R -> S (IN SITOSTEROLEMIA).	L-> P (IN SITOSTEROLEMIA).	(IN SITO	
	577	549	499 535	475	446	2	390	σ.	_	294 314	o un	234	194	174	134	115	75	64	16												

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578 INLSSLWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVS 625

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structure and spectrum of mutations involving sterolin-2, encoded by ABCG5 and ABCG8, respection. J. Hum. Genet. 69:278-290(2001).
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                                                                                                                                                              TRANSMEM
                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                PROSITE; PS00211; ABC_TRANSPORTER; 1
                                                                                                                                                                                                                                                              SMART; SM00382;
                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                  VARSPLIC
                                                                                                  DOMAIN
                                                                                                           TRANSMEM
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                                                                                                                                    TRANSMEM
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                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                            EMBL; AF351785; AAK84831.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka
Ose L., Stalenhoef A.F.H., Mietinnen T., Bjorkhem I.,
Pandya A., Brewer H.B. Jr., Salen G., Dean M., Srivas:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague-Dawley;
MEDLINE-21344600; PubMed-11452359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniaca; vezo
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P58428;
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patel S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Two genes that map to the STSL locus cause sitosterolemia: genomic structure and spectrum of mutations involving sterolin-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG8_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                CAUTION: Seems to have a defective ATP-binding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           produced by SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: May form heterodimers with ABCG5 or be tightly ABCG5 along a pathway regulating diatery-sterol absorptiexcretion (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the
                                                                                                                                                                                                                                                                       PF00005; ABC_tran;
                                                                                                                                                                                                                                                                                 IPR003593; AAA_ATPase.
IPR003439; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                into bile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 41, Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cassette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel.
                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                           AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                         376
75878
 20
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Last annotation update)
sub-family G, member 8 (Sterolin-2)
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%
;
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Score
Pred.
                                 N-LINKED (GLCNAC. . .)
MISSING (IN ISOFORM 2).
6088973F3FA4C36F CRC6
                                                                      CYTOPLASMIC
                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                       CYTOPLASMIC
                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                   Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and ABCG8, respectively.";
                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                  (POTENTIAL)
                                                                                                             (POTENTIAL)
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691;
No.
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                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
 9
                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ng as its content is in
DB 1;
).8e-41;
                                                                                                                                                                                                                                Alternative splicing.
                                            (POTENTIAL).
                                                                                                                    (POTENTIAL).
                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                         Usage
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        Length
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Bruckert E.,
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                                                                                                                                                               Q9UNQO; Q95374; Q9NUSO; Q9BY73;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP-binding cassette, sub-family G, member 2 obinding cassette transporter) (Breast cancer ABCG2 OR ABCP OR BCRP OR BCRP1.
                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                       ABG2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                         633
                                                                                                                                                                                                                                                                                                                                                                                                       602
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                                                                                                                                                                                                                                                                                                                                               -LIVIGI 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDSWDLGI-RNLSFKVRSGQMLAIIGSAGCGRATLLDVITGRDHGGKMKSGQIWINGQPS
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                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126;
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                                                                                                                                                                              (Placenta-specific ATP-resistance protein).
                                                                                                                                                                                                                                                                                                                                                                                                    -PGDAMVTAMDLNSHPLYAIY-
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Allikmets R., Schriml L.M., Hutchinson A., Roman "A human placenta-specific ATP-binding cassette chromosome 4q22 that is involved in multidrug re Cancer Res. 58:5337-5339(1998).

Romano-Spica V.,

resistance gene

(ABCP)

9 Dean MEDLINE=99065313; PubMed=9850061;

TISSUE≃Placenta;

SEQUENCE FROM N.A.

NCBI_TaxID-9606; Mammalia; Eutheria; Homo sapiens (Human)

Eukaryota; Metazoa;

Primates; Chordata;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

resistance

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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara P. Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watahashi M., Chiba Y., Ishida S., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamata A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Ninomiya K., Iwayanagi T., Shiba Y., Iwayanagi T., Iwayanagi T., Iwayanagi T., Iwayanagi T., Iwayanagi T., Iwayanagi T., Iwayanag
ATP-binding; Transmembrane;
DOMAIN 1 395
TRANSMEM 396 416
DOMAIN 417 428
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                          Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr;
                                                                              PROSITE;
                                                                                                SMART; SM00382; AAA;
                                                                                                                                                    InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transpo
                                                                                                                                                                                             Genew; HGNC:74; ABCG2
MIM; 603756; -.
                                                                                                                                                                                                                                 EMBL; AF103796; AAD09188.1;
EMBL; AF098951; AAC97367.1;
EMBL; AB056867; BAB39212.1;
EMBL; AK002040; BAA92050.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21474438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 198-655 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A multidrug resistance transporter from human MCF-7 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ross D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Breast cancer resistance protein homodimer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kage K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doyle L.A.,
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MEDLINE-99080071; PubMed-9861027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY.
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                                                                          PS00211; ABC_TRANSPORTER; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsukahara S.,
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; BAB39212.1;
; BAA92050.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-11590207;
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                                                                                                                                                      transportr.
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                  CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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                                                                           HRMLPSIIFTCIVYEMLGLKPKADAFFVMMFTLM---WAYSASSMALAIAAGQSVVSVA
 LNATGNNPCNYA---
                                    TLLMTICEVEWMIESGLLVNLTTIASWLSWLQYFSIPRYGETALQHNEELGQNECPG---
                                                                                        FSVVATMIFSSVCYWTLGLHPEVAREGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSV 533
                  VSVTTNPMCAFTQGIQFIEKTCPG
                                                        VALLSIAGV--LVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSN
                                                                                                                   GIQNRAGVLF-FLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP
                                                                                                                                      AIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYAL-HVLP
                                                                                                                                                                           KTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFL--LFFVLRVRSNVLKG
                                                                                                                                                                                                  EEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKKITVFKEISY
                                                                                                                                                                                                                                          FKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIINGDSTAVALNR
                                                                                                                                                                                                                                                    FQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQ----SK
                                                                                                                                                                                                                                                                                ERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSEL
                                                                                                                                                                                                                                                                                                                      VMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIEELGLDKVADSKVGTQFIRGVSGG
                                                                                                                                                                                                                                                                                                                                                                           TT----SFCHQLRWYSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDST----
                                                                                                                                                                                                                    ERE-----IETSKR-----VQMIESAYKKSAICHKT-----LKNIERMKHLKTLPMVPF
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                                                                                                                                                                                                                                                                                                                                                                                                                          SQSSLEGAPATAP---EPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVE
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72343 MW;
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N-LINKED (GLCNAC. . .) (POT
N-LINKED (GLCNAC. . .) (POT
V -> A (IN REF. 2 AND 4).
E -> Q (IN REF. 2 AND 4).
F -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 9.8e7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 676.5; DB 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING
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RESULT 8
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ID YOH5_YEAST

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01-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
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CARBOHYD
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                   CARBOHYD
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EMBL; Z74816; CAA99084.1; -.
SGD; S0005435; YOL075C.
                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tzermia M., Katsoulou C., Alexandraki D.:
"Sequence analysis of a 33.2 kb segment from the left arm of yeast chromosome XV reveals eight known genes and ten new open reading frames including homologues of ABC transporters, inositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement
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Yeast 13:583-589(1997)
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                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97321807; PubMed=9178509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probable ATP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                     120
                                       706
                                                          65
                                                                                   Similarity
VSELMFKNVCSYVSQDDDHLLAALTVKETLKYAAALRLHHLTEAERMERTDNLIRSLGLK
            TREILQSVNAIFKPGMINAIMGPSGSGKSSLLNLISGRL-KSSVFAKFDTSGSIMFNDIQ 764
                                                TRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFL-----GEVYVNGRA
                                                                                                                                                                                                                                                                                                                                     PD000006; ABC_
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IPR003439; ABC_transportr.
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                                                                           Conservative
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Last annotation update)
t transporter YOL074C/YOL075C
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                                                                                 Score 627; DB 1;
Pred. No. 6.7e-36;
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                                                                                                                                                                                                                       (POTENTIAL).
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    Transmembrane; Glycoprotein;

                                                                                                                                                        (GLCNAC. .
                                                                                                                      (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                               (GLCNAC
                                                                                                                                         (GLCNAC
                                                                                                                                                 (GLCNAC
                                                                          228;
                                                                                          Length 1294;
                                                                        Indels
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) (POTENTIAL).
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Elizur A., Vacek A.T., Howells A.J.;

"Cloning and characterization of the white and topaz eye color genes from the sheep blowfly Lucilia cuprina.";

J. Mol. Evol. 30:347-358(1990).

-i- FUNCTION. MAY BE PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY FOR THE TRANSPORT OF PIGMENT PRECURSORS INTO PIGMENT CELLS RESPONSIBLE FOR EYE COLOR.

-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SUBCELLULAR LOCATION: Integral membrane protein. 01-FEB-1995 01-NOV-1997 16-OCT-2001 This MEDLINE=97087158; PubMed=8933176; Garcia R.L., Perkins H.D., Howells A.J.; "The structure, sequence and developmental pattern the white gene in the blowfly Lucilia cuprina."; Insect Mol. Biol. 5:251-260(1996). Eukaryota; Metazoa; Arth Insecta; Pterygota; Neopi Muscomorpha; Oestroidea; LUCCU 005360; WHIT_LUCCU MEDLINE=90264941; PubMed=1971656; SEQUENCE OF 490-584 FROM N.A. SEQUENCE FROM N.A. Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly). Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; He 9 SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics (Rel. 31, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat STANDARD; Arthropoda; Mandibulata; Neoptera; Endopterygota; idea; Calliphoridae; Lucij PRT; It is produced through a collaboration informatics and the EMBL outstation 677 update) Lucilia æ Diptera; Brachycera; of. expression Hexapoda; œ,

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ProDom; PD000006; ABC_transportr;

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InterPro; InterPro; InterPro;

IPR003593; AAA_ATPase.
IPR003439; ABC_transportr.
IPR005284; Pigment_permease.

X53265;

CAA37365.1;

U38899; AAA82057.1;

Pigment; NP_BIND

ATP-binding; Transmembrane; PS00211; ABC_TRANSPORTER; 1

Transport.

PROSITE; TIGRFAMS; SMART;

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titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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"The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of chromosome III from Saccharomyces cerevisiae reveals seven open reading frames including the RVS161, ADP1 and PGK genes."; Yeast 8:409-417(1992).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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InterPro; IPR003439; ABC_transportr.
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"The product of the YCR105 gene located on the chromosome III
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Saccharomycetales;
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16-OCT-2001 (Rel. 40, Last annotation update)
Probable ATP-dependent permease precursor.
ADP1 OR YCR011C OR YCR11C OR YCR105.
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    SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                   Anopheles gambiae (African malaria mosquito). 
Eukaryota; Metazoa; Arthropoda; Mandibulata; 
Insecta; Pterygota; Neoptera; Endopterygota; 
Culicoidea; Anopheles.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LAYYISKIMSEVVPLRVVPPILLSLIVYPMTGLNMKDNAF-FKCIGILILFNLGISLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMLAYAL-----HVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NV-SNDISG-FQNRMGLFFFILTYFGFVTFTGL----SSFALERIIFIKERSNNYYSP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVRSNVLKGAIQDRVGLLY---QFVGATFYTGMLNAVNLFFVLRAVSDQESQDGLYQKWQ
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28.6%;
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MW; ABC9CE54BCFDF6A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 621; DB 1;
Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                       648
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                                                                                                    Pancrustacea; Hexapo Diptera; Nematocera;
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                                                                                                                      Hexapoda;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR005284; Pigment_permease.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U29486; AAC46995.1; -. EMBL; U29485; AAC46994.1; -. EMBL; U29484; AAC47423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Besansky N.J., Bedell J.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and characterization of the white gambiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins F.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insect Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96423158; PubMed=8825759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ect Mol. Biol. 4:217-231(1995).

FUNCTION: MAY BE PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY FOR THE TRANSPORT OF PICHENT PRECURSORS INTO PIGMENT CELLS RESPONSIBLE FOR EYE COLOR.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                       275
                                                                                                                                                                                          224
                                                                                                                                                                                                                                                                                                                                                                                                                                                        170;
                                                                                                                                                                                                                                                                                                                                                                                96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD000006;
                                                                                                                                                                                                                                                      QKKVEAVMAELSLSHVADRLIGNYS-LGGISTGERRRVSIAAQLIQDPKVMLFDEPTTGL
                                                                                                                                                                                                                                                                                                                                                                                            TSCROQWTRQ-----ILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGT
                                      RMKHLKTLPMVPFKTKDSPGVFSKL-GV-----
                                                                       FSQLGIPCPPNYNPADFYVQMLAI---APAKEAECRDMIKKICDSFAVSPIAREVLETAS
                                                                                               ENDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIE
                                                                                                                                               DSFMAHSVLQVLKGMAMKGKTIILTIHQPSSELYCLFDKILLVAEGRVAFLGSPYQSAEF
                                                                                                                                                                  QHRVQEVLQELSLVKCADTIIGAPGRIKGLSGGERKRLAFASETLTDPHLLLCDEPTSGL
                                                                                                                                                                                                                                                                                                KISPNAVRALNGVPVNAEQLRARCAYVQQDDLFIPSLTTREHLLFQAMLRMGRDVPASVK
                                                                                                                                                                                                                                                                                                                      FLGEVYV---NGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSF-
                                                                                                                                                                                                                                                                                                                                                                          TRLRNCCTRQRKDFNPRKHLLKNVTGVAKSGELLAVMGSSGAGKTTLLNALAFR-SPPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABC_TRANSPORTER; 1.
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VAGKGMDEPYMLQQVEGVGSTGYRSSWWTQFYCILWRSWLSVLKDPMLVK
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295
464
494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Benedict M.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 607.5; DB 1; Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRS -> YAR (IN REF. 1; cm;
; EE8B9517239B2961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-> S (IN REF 1, AAC47423).
SRS -> YAR (IN REF. 1; AAC47423).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      208;
                                  ------LLRRYTRNLVRNKLAVI
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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W OR EG:BACN33B1.1 OR CG2759
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ASZTALOS Z., AWANO
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PIR;

S08635; S08635

FlyBase;

FBgn0003996; ; IPR003593; /

IPR003593; AAA_ATPase.
IPR003439; ABC_transportr.

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Genetics 122:595-606(1989).

-I- FUNCTION: PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY
FOR THE TRANSPORT OF PIGMENT PRECURSORS INTO PIGMENT CELLS
RESPONSIBLE FOR EYE COLOR. WHITE DIMERIZE WITH BROWN FOR THE
TRANSPORT OF GUANINE AND WITH SCARLET FOR THE TRANSPORT OF
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                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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PROSITE; PS00211; ABC_TRANSPORTER; 1.
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                  FIP----ALVILGIVVFKIRDHLISR
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130 137 ATP (BY SIMILARITY).
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A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
A Menzel U., Delabar J., Kumpf K.; Lehmann R., Patterson D.,
A Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
A Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
A Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
The DNA sequence of human chromosome 21.*;
Nature 405:311-319(2000).
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P45844; Q9BXLO; Q9BXL1;
Q9BXK8; Q9BXK9;
Q1-NOV-1995 (Rel. 32, Ct)
15-JUN-2002 (Rel. 41, Lt)
15-JUN-2002 (Rel. 41, Lt)
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE-21192304; PubMed-11279031;

Porsch-Oezcueruemez M., Langmann T., Heimerl S., Borsukova H.,

Kaminski W.E., Drobnik W., Honer C., Schumacher C., Schmitz G.;

"The zinc finger protein 202 (ZNR202) is a transcriptional repressor

of ATP binding cassette transporter Al (ABCA1) and ABCG1 gene

expression and a modulator of cellular lipid efflux.";

J. Biol. Chem. 276:12427-12433(2001).
                              Croop J.M., T
Goldenson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE-20408883; PubMed-10950923;

Berry A., Scott H.S., Kudoh J., Talior I., Koros
Wattenhofer M., Guipponi M., Barras C., Rossier

Mattenhofer M., Guipponi M., Barras C., Rossier
        MEDLINE-97186700; PubMed-9034316;
Croop J.M., Tiller G.E., Fletcher
Goldenson D., Archiegas S., Son
"Isolation and characterization of
                                                                                                                                                                                              Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Refined localization of autosomal recessive nonsyndromic deafness DFNBIO locus using 34 novel microsatellite markers, genomic structure, and exclusion of six known genes in the region."; Genomics 68:22-29(2000).
                                                                                                                 TISSUE=Fetal brain;
                                                                                                                                             SEQUENCE OF 33-678
                                                                                                                                                                                                                                                Lorkowski S., Rust S., Engel Assmann G., Cullen P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang J., Kawasaki K., Asakawa S., Minoshima
Antonarakis S.E., Bonne-Tamir B.;
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MEDLINE-20289799; PubMed-10830953;
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Chen H.M., Rossier C., Lalioti M.D.,
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ABCG1 OR ABC8 OR WHT1.
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of a mammalian
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ssier C., Shibuya
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"Role of ABCG1 and other ABCG family members in lipid metabolism.";
J. Lipid Res. 42:1513-1520(2001).
-!- FUNCTION: Transporter involved in macronhage limid homococcu-
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Porsoft-Oezcueruemez M., Liebisch G., Kapinsky M., Diederich W.,
Drobnik W., Dean M., Allikmets R., Schmitz G.,
*ABCG1 (ABC8), the human homolog of the Drosophila white gene, is
regulator of macrophage cholesterol and phospholipid transport.",
proc. Natl. Acad. Sci. U.S.A. 97:817-822(2000).
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Mangelsdorf D.J.,
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Gene 185:77-85(1997).
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MEDLINE=20105556; PubMed=10639163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20261604;
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                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. The by non-profit institutions as long filed and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDUCTION: Strongly induced in monocyte-derived macrophages cholesterol influx. Conversely, mRNA and protein expression suppressed by lipid efflux. Induction is mediated by the liver X receptor/retinoide X receptor (LXK/RXR) pathway.

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WH.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: At least 7 isoforms; 1 3/ABDE, 4/6, 5/F, 6/HI and 7/C; are produced splicing and alternative initiation. TISSUE SPECIFICITY: EXPRESSED IN SEVERAL TISSUE SPECIFICITY: EXPRESSED IN SEVERAL TISSUE SPECIFICITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the ABCG subfamily. SUBCELLULAR LOCATION:
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                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                          Science 270:2005-2007(1995).

-I- FUNCTION: MAY BE PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY FOR THE TRANSPORT OF PIGMENT PRECURSORS INTO PIGMENT CELLS RESPONSIBLE FOR EYE COLOR.

-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
 Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr;
ProDoms: TIGR00955; 3a01204; 1.
                                                                                                                                                                                                                                                      Zwiebel L.J., Saccone G., Zacharopoulou A., Besansky
Favia G., Collins F.H., Louis C., Kafatos F.C.;
"The white gene of Ceratitis capitata: a phenotypic m
germline transformation.";
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-96123276; PubMed-8533095;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997
16-OCT-2001
                                   InterPro; IPR003439; ABC_transportr.
InterPro; IPR005284; Pigment_permease.
                                                                 EMBL; X89933; CAA61998.1;
                                                                                                                                                                                                                                                                                                                                                                                   Ceratitis capitata (Mediterranean fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                          White protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPGATSRFTMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMGVELREHLNYWYSLKAYYLAKTMADVPFQIMEPVAYCSIVYWMTSQPSDAVREVLFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTHLRITSHIGIGLLIGLLYLGIGNEAKK--VLSNSGFLFFSMLFLMFAALMPTVLTFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHRPSEEVKQTKRLKGL-----RKDSSSMEGCHSFSASCLTQFCILFKRTFLSIMRDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHKTLKNIERMKHLKTLPMVPFKTKDSPGV------FSKLGVLLRRVTRNLVRNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRDLGLNCPTYHNPADFVMEVASGEYGDQNSRLVRAVREGMCDSDHKRDLGGDAEVNPFL
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40,
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, Last annotation
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Best Local
                    ABG4_HUMAN S
Q9H172;
15-JUN-2002 (Rel
15-JUN-2002 (Rel
15-JUN-2002 (Rel
15-JUN-2002 (Rel
ATP-binding cass
ABCG4 OR WHITE2.
                                                                                                        HUMAN
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CARBOHYD
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Pigment;
NP_BIND
TRANSMEM
TRANSMEM
Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
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                             (Rel. 41, Created)
(Rel. 41, Last sequence up
(Rel. 41, Last annotation
cassette, sub-family G, me
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Similarity
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                          FIP-ALVILGIVVFKIRDHL 648
                                                                                   NEFYGL---NETCGSSNVSVTTNPMCAFTQGIQFIEKTCP--GATSRFTMNFL---ILYS
                                                                                                                 GYLISCACSSTSMALSVGPPVIIPFLLFGGFFLNSGSVPVYFKWLSYLSWFRYANEGLLI
                                                                                                                                                                            LFLVVPFLFTAIAYPLIGLRPGVDHF------FTALALVTLV--ANVSTSF
                                                                                                                                                                                                        FSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSV
                                                                                                                                                                                                                                                                  GAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLP
                                                                                                                                                                                                                                                                                                ENEYTYKASWEMQERAVLWRSWLSVLKEPLLVKVRLLQTTMVAVLIGLIFLGQQLTQV--
                                                                                                                                                                                                                                                                                                                                                            YVQVLAV---VPGREVESRDRVAKICDNFAVGKVSREMEQNFQ-----KLVKSNGFGKED
                                                                                                                                                                                                                                                                                                                                                                                          YMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKD
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ATP-bindi
121
427
457
507
508
568
651
                                                          NQWADVKPGEITCTLSNT-
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643
679
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525
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586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 591; DB 1;
Pred. No. 9.4e-34
25; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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POTENTIAL.
669
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                                                                                                                                              IAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVV
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-LINKED (GLCNAC. . .) (POTENTIAL)
3F9CBC78A835C4CC CRC64;
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                                                          -TCPSSGEVILETLNFSASDLPFD
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STANDARD;

PRT;

646

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Chordata; Craniata; Vertebrata; Euteleostomi;

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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PDUUUUUL, AA; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 20-646 FROM N.A.

TISSUE-Dorsal root ganglion;
Oldfield S., Lowry C.A., Lightman S.L.;
*Cloning and expression of a novel mammalian white family
*BBC-transporter: WHITE2 *;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
*I- FUNCTION: May be involved in macrophage lipid homeostasis.
*I- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
*I- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                               NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21518231; PubMed=11606068;
Engel T., Lorkowski S., Lueken A., Rust S., Schlueter B., Berger G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ300465; CAC17140.1; -. Genew; HGNC:13884; ABCG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                           MAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                     RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFAMILY.
207 LLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAIL 266
                                                                                                                                                                                                          171;
                                   167
                                                      153 LLAIRRGNPGSFQKKVEAV-----MAELSLSHVADRLIGNYSLGGISTGERRRVSIAAQ
                                                                                                                     93
                                                                                                                                                                             33
                                                                                                                                                  54
                                                                                                                                                                                                                     Similarity
                                                                                                               TTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTA 152
                                                                                                                                                                       PEPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSSGSGK 92
                            NLKLSEKQ----EVKKELVTEILTALGLMSCSHTRTAL-----LSGGQRKRLAIALE
                                                                                     STFMNILAGY -- RESGMKGQILVNGRPRELRTFRKMSCYIMQDDMLLPHLTVLEAMMVSA 166
                                                                                                                                             PKRSAVDIEFVELSYSVREGPCW-----RKRGYKTLLKCLSGKFCRRELIGIMGPSGAGK 108
                                                                                                                                                                                                                                                                 422
646 AA;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  494
                                                                                                                                                                                                                     17.48;
27.18;
                                                                                                                                                                                                                                                                  71895 MW;
                                                                                                                                                                                                          126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Transport.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                     Score 578.5; |
Pred. No. 6.6e
26; Mismatches
                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
9CCEC6E150772611 CRC64;
                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL):
                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no
                                                                                                                                                                                                                      .6e-33;
                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as its content
                                                                                                                                                                                                       274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                 Length 646;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
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                                                                                                                                                                                                    Gaps
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                            214
                                                        206
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Séarch completed: June 11, 2003, 09:12:37 Job time : 18 secs

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Total number of hits satisfying chosen parameters:
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Pred. No. is the number of results predicted by chance to l score greater than or equal to the score of the result being and is derived by analysis of the total score distribution
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

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25-SEP-2001; 2001WO-US29859.

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04-APR-2002.

(USSH) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B. (DEAN/) DEAN M.

ABCG5 mutant

Description Human ABCG5

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c-differ	o sapiens.	Human; ABCG5; ATP arteriosclerosis; chromosome 2p21.	Human ABCG5	30-JUL-2002	AAU96984;	96984		463.5	515.5	553	569.5	5/5.5 571	575.5	578	578.5	587.5	587.5	588 5	602.5	672.5	674.5	674.5	680.5	680.5	680.5	682.5	722	1234	→ 6	2727.5	
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lifiers led by GGTCTC"		g cassette gene 5; sitoste disease; hypersterolemia;				651 AA.	ALIGNMENTS	ABB64565	ABB59544	ABB60524	ABB57112	AAG43099 ABB64566	AAG43100	ABP61858	AA014186	AAG18079 AAY78981	AAG18080	ABB65432	ABB07272 ABB59384	ABB07273 ABB07273	AAU04348	AA014783 AAY95365	AA014782	AAU80028	AAB60104	AAU80029	AAB41856	AAU96988	699	AAU96986	
	٠	sitosterolemia; cholesterol; lemia; Alzheimer's disease;						Drosophila melanog Drosophila melanog		Arabidopsis thalia Drosophila melar.r	Mouse ischaemic co	Arabidopsis thalia	Arabidopsis thalia	Human secreted pro	Human transporter		Arabidopsis thalia	' = :	Murine BCRP (mBCRP	Human BCRP (huBCRP	n BCRP/	Human BCRP-related	Human BCRP-related		Human transport pr	ABCG2 mutan		Human ABCG5 mutant		Rat ABCG5 protein.	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying CC a compound which alters ABCG5 activity level comprising contacting a cell CC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal. CC where an increase or decrease in ABCG5 biological activity in a control cell culture or mammal not CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC elimilation of ABCG5 activity is useful for treating or preventing CC stimulation of ABCG5 activity is useful for treating or preventing CC disease. The method of the invention is useful for increasing cholesterol active or mammal abCG5 polypeptide. The method of the invention is useful for the invention. This sequence is encoded by the human ABCG5 protein of the invention. This
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Best Local
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                                                                                                                            SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRV
                                                                                                                                                                  ADRLIGNYSLGGISTGERRRYSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR 240
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GLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATM
                                                                                                             SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRV
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                                                                                                                                                                                                          (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) binding cassette (ABC) family cholesterol transporter. SSG is useful for identifying a compound useful in the treatment or prevention of a sterol-related disorder, including sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or nutritional deficiencies. SSG is also useful for treating cholesterol-associated diseases or conditions including coronary heart disease and other cardiovascular diseases, and sitosteroleemia-associated condition including arthritis, xanthomas and chronic haemolytic anaemia. SSG expression cassette is useful in the production of transgenic non-human animals. SSG genes and their homologues are useful as tools for a number
                                                                        of applications including diagnosing sitosterolaemia and other cardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The present sequence is human SSG protein. Human SSG is located on chromo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel sitosterolemia susceptibility gene polypeptide and polynucleotide, useful for screening a compound that increases the level of expression or activity of SSG polypeptide for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated Sitosterolaemia Susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 19; Fig
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xanthoma; haemolytic anaemia;
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Query Match
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Score 3326; Pred. No. 0; 0; Mismatches

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                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                      ATP-binding cassette gene 5; sitosterolemia; cholesterol; is; heart disease; hypersterolemia; Alzheimer's disease;
                                                                  /note-
                                                             "Wild-type Glu
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a compound which alters ABGGS activity level comprising contacting a cell culture or mammal which have ABGGS polypeptide with a compound and measuring ABGGS biological activity in the cell culture or in mammal, where an increase or decrease in ABGGS biological activity compared to ABGGS biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or decreases ABGGS activity respectively. The cell culture or mammal comprises a mutated ABGGS polypeptide or a wild type polypeptide. The ABGGS biological activity, or level of ABGGS mRNA, or level of the polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal comprising a wild type ABCGS polypeptide. Stimulation of ABCGS activity is useful for treating or preventing the presenting contacterol activity is contacted activity in the cell culture or mammal comprising cholesterol activity is seful for increasing cholesterol activity is contacted activity in the cell culture or mammal is also activity contacted activity in the cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal comprision is compared with that of a second cell culture or mam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel mammalian ATP-binding cassette gene 5 polypeptide, nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                  of the specification.
                                                                                        Note: This sequence is not shown in the specification but is derived from the wild type human ABCG5 protein (AAU96984) given on pages 35-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B.
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Query Match Best Local Matches

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Conservative

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Similarity

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SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLELLFFVLRVRSNVLKGAIQDRV
                                                                                             RNRIVVLT IHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDF
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                                                YMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKD
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XW Huma
XW Huma
XW Bite
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The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or mammal
                                                                                                                                                                                                    Novel mammalian ATP-binding cassette gene 5 polypeptide, and the nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
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(PATE/) PATEL S B.
(DEAN/) DEAN M.
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RESULT 5
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AC AAU9
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DT 30-J
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AAU96990;

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30-JUL-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the specification.
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            AFTQGIQFIEKTCPGATSRFTMNFLILYSFIPALVILGIVVFKIRDHLISR
                                              AFTQGIQFIEKTCPGATSRFTMNFLILYSFIPALVILGIVVFKIRDHLISR
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                  decreases ABCG5 activity respectively. The cell culture or manual comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The ABCG5 biological activity, or level of ABCG5 mRNA, or level of the polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal comprising a wild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present amino acid sequence represents the human ABCG5 mutant R389H protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     where an increase or decrease in ABCG5 biological activity compared ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or contacted with the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                   Note: This sequence is not shown in the specification but is derived from the wild type human ABCG5 protein (AAU96984) given on pages 35-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page -; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel mammalian ATP-binding cassette gene 5 polypeptide, an nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not
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(PATE/) PATEL S B.
(DEAN/) DEAN M.
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Protein; 651 Ā

Human ABCG5 mutant R419P protein sequence

ATP-binding cassette gene 5; sis; heart disease; hyperstero hypersterolemia; sitosterolemia; cholesterol;
olemia; Alzheimer's disease;

Location/Qualifiers

/note= "Wild-type Arg substituted Ьy

2001WO-US29859

25-SEP-2000; 2000US-235268P

(USSH) US DEPT HEALTH & HUMAN SERVICES. (PATE/) PATEL S B. (DEAN/) DEAN M.

WPI; 2002-416483/44

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying a cCC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal, which have ABCG5 polypeptide with a compound and CC where an increase or decrease in ABCG5 biological activity compared to CC ABCG5 biological activity in a control cell culture or mammal not CC contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or mammal CC Comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mid type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal is also compared with that of a compound cell culture or mammal i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is not shown in the specification but is derived the wild-type human ABCG5 protein (AAU96984) given on pages 35-
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                    (SSG) polypeptide. SSG is a member of adenosine triphosphate (APP) CC binding cassette (ABC) family cholesterol transporter. SSG is useful CC for identifying a compound useful in the treatment or prevention of a Sterol-related disorder, including sitosterolaemia, hyperlipidaemia, hyperricholesterolaemia, gall stones, HDL deficiency, atherosclerosis or cutritional deficiencies. SSG is also useful for treating cholesterol-cc associated diseases or conditions including coronary heart disease and cother cardiovascular diseases, and sitosterolaemia-associated condition including archritis, xanthomas and chronic haemolytic anaemia. SSG expression cassette is useful in the production of transgenic non-human complete the conditions including diagnosing sitosterolaemia and other cardiovascular disorders, for forensics and paternity determinations, candinals. SSG genes and their homologues are useful as tools for a number cardiovascular disorders, for forensics and paternity determinations, candiovascular disorders, for forensics and paternity determinations, and cortest sequence is mouse SSG protein variant obtained by replacing the present sequence is mouse SSG protein variant obtained by replacing
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel sitosterolemia susceptibility gene polypeptide and polynucleotide, useful for screening a compound that increases the level of expression or activity of SSG polypeptide for treating
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               The invention relates to an isolated Sitosterolaemia Susceptibility Gene (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) binding cassette (ABC) family cholesterol transporter. SSG is useful for identifying a compound useful in the treatment or prevention of a sterol-related disorder, including sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or nutritional deficiencies. SSG is also useful for treating cholesterolaesosciated diseases or conditions including coronary heart disease and other cardiovascular diseases, and sitosterolaemia-associated condition including arthritis, xanthomas and chronic haemolytic anaemia. SSG expression cassette is useful in the production of transgenic non-human expression cassette is useful in the production of transgenic non-human
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useful in the production of
their homologues are useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of applications including diagnosing sitosterolaemia and other cardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The present sequence is mouse SSC protein variant obtained by replacing liel7 with Leu.
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                                                                                     VADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELA
                                                                                                                                                                                                                                                                                                                                                                                                                                         MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEP-HSLGILHASYSVSHRVRPWWDITS 59
                                          SGLLIGSGFIRNIQEMPIPLKILGYFTFQKYCCEILVVNEFYGLNFTCGGSNTSMLNHPM
                                                        AGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSYTTNPM
                                                                                                                                                                           DPPGMFGKLGVLLRRVTRNLMRNKQAVIMRLVQNLIMGLFLIFYLLRVQNNTLKGAVQDR
                                                                                                                                                                                        DSPGVFSKIGVLLRRYTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDR
                                                                                                                                                                                                                       FYMDLTSVDTQSREREIETYKRVQMLECAFKESDIYHKILENIERARYLKTLPMVPFKTK
                                                                                                                                                                                                                                 FYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTK
                                                                                                                                                                                                                                                                 RRDRIVIVTIHOPRSELFOHFDKIAILTYGELVFCGTPEEMLGFFNNCGYPCPEHSNPFD
                                                                                                                                                                                                                                                                             RRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFD
                                                                                                                                                                                                                                                                                                           VADQMIGSYNFGGISSGERRRVSIAAQLLQDPKVMMLDEPTTGLDCMTANQIVLLLAELA
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Pred. No. 4.7e-280;
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RESULT 10
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AAU96985 standard;
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Protein;

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AAU96985

30-JUL-2002 (first

Mouse ABCG5 protein.

Mouse; ABCG5; ATP-binding cassette gene 5; sitosterolemia; arteriosclerosis; heart disease; hypersterolemia; Alzheimen Alzheimer' cholesterol; s disease.

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                                                                                                                                                                                                                                                                                                                                             The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell CC unture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal, CC where an increase or decrease in ABCG5 biological activity on a control cell culture or mammal not CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mammal is also compared with that of a second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is useful for treating or preventing CC disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present amino CC acid sequence represents the mouse ABCG5 protein of the invention.
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Best Local Similarity
Matches 522; Conser
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel mammalian ATP-binding cassette gene 5 polypeptide, nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 42; 66pp; English.
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                          LRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSH 179
                                                                                                                                                MGELPFLSPEGARGPHINRGSLSSLEQGSVTGTEARHSLGVLHVSYSVSNRVGPWWNIKS
RRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFD
                                                                                       LRRDQFQDCFSYVLQSDVFLSSLTVRETLRYTAMLALCRSSADFYNKKVEAVMTELSLSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPPGMFGKLGVLLRRVTRNLMRNKQAVIMRLVQNLIMGLFLIFYLLRVQNNTLKGAVQDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYMDLTSVDTQSREREIETYKRVQMLECAFKESDIYHKILENIERARYLKTLPTVPFKTK
                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                           hypersterolemia;
                                                                                                                                                                                                                                                                 5; sitosterolemia;
                                                                                                                                                                                                                                                          Alzheimer's
                                                                                                                                                                                                                                                                  cholesterol;
                                                                                                                                                                                                                                                          disease
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25-SEP-2001; 2001WO-US29859

25-SEP-2000; 2000US-235268P

(USSH) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B. (DEAN/) DEAN ×

Patel SB, Dean M;

WPI; 2002-416483/44. ABK51686.

Novel mammalian ATP-binding cassette gene 5 puncleic acid encoding the polypeptide, useful sitosterolemia, arteriosclerosis and heart di heart diseases polypeptide, ul for treati treating

Example Ψ Page 45; 66pp; English.

The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or hear disease. The molecules of the invention are also useful for identifyin a compound which alters ABCG5 activity level comprising contacting a culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity 'n lerosis or heart for identifying contacting a cell 얁

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RESULT 12
AAU96991
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or mammal comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The ABCG5 biological activity, or level of ABCG5 mRNA, or level of the polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal comprising a wild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present amino acid sequence represents the rat ABCG5 protein of the invention.
         30-JUL-2002
                              AAU96991;
                                                 AAU96991 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                 LRREOFODCFSYVLOSDTLLSSLTVRETLHYTALLAIRRGNPGSFOKKVEAVMAELSLSH
                                                                                                                                       SGLLIGSGFIRNIEEMPIPLKILGYFTFQKYCCEILVVNEFYGLNFTCGGSNTSVPNNPM
                                                                                                                                                   AGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPM
                                                                                                                                                                                                                                                                                                                                                                                                     VADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELA
                                                                                                                                                                                                                                                                                                                                                                                                                                   LRRDQFQDCVSYLLQSDVFLSSLTVRETLRYTAMLALRSSSADFYDKKVEAVLTELSLSH
                                                                                                                                                                                                                                                                                                                                                                                            VADQMIGNYNFGGISSGERRRVSIAAQLLQDPKVMMLDEPTTGLDCMTANHIVLLLVELA
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        (first entry)
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                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2727.5; DB 23
Pred. No. 1.8e-278;
Pred. No. 1.8e-278;
                                               Å
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61

RQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRAL 120

MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSC

Matches Query Match Best Local

Similarity

62.6%; illarity 100.0%; Conservative

· 0;

Score 2081; DB 23; Pred. No. 1.7e-210; Mismatches

Length Indels

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Gaps

60 60 Sequence

408 AA;

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The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for, identifying CC a compound which alters ABCG5 activity level comprising contacting a cell CC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal. CC where an increase or decrease in ABCG5 biological activity compared to CC ABCG5 biological activity in a control cell culture or in mammal not CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC ABCG5 biological activity is useful for treating or preventing CC second cell culture or mammal comprising a wild type ABCG5 polypeptide. The CC Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell cult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel mammalian ATP-binding cassette gene 5 polypeptide, and nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                     Note: This sequence is not shown in the specification but is derived from the wild type human ABCG5 protein (AAU96984) given on pages 35-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page -; 66pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B. (DEAN/) DEAN M.
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                                                                                                                                invention.
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       The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or mammal comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The
                                                                                                                                                  Novel mammalian ATP-binding cassette gene 5 polypeptide, nucleic acid encoding the polypeptide, useful for treatisitosterolemia, arteriosclerosis and heart diseases
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(PATE/)
(DEAN/)
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                                                                                                                                                                                                                                                                                                                                                      Cricetinae sp.
                                                                                                                                                                                                                                                                                                                                                                    Hamster; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease.
                                                                                                                                  Example 3; Page 46; 66pp; English.
                                                                                                                                                                                                                      Patel SB, Dean M;
                                                                                                                                                                                                                                                                                                                    04-APR-2002
                                                                                                                                                                                                                                                                                                                                      WO200227016-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU96987 standard; Protein;
                                                                                                                                                                                            N-PSDB; ABK51687.
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                                                                                                                                                                                                                                                                                                                                                                                                     Hamster ABCG5
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DEAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVR 408
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 Patel SB,
                  (USSH ) US DEPT HEALTH & HUMAN (PATE/) PATEL S B. (DEAN/) DEAN M.
                                                                          25-SEP-2001;
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                                                                                                                                                                      Synthetic.
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Dean M;
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polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal comprising a wild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents the hamster ABCG5 protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                      TLKNIERMKHLKTLPMVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMG
                                                                                                                                                                                                   AEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHK
                                                                                                                                                                                                                                                                                                                                                                                                                                               AISGRLRRTGTLEGEVFVNGRELRRDQFQDCFSYVLQSDVFLSSLTVRETLRYTAMLALR
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                       LELLEFVLRVRSNVLKGAIQDRVGLLYQFVGATPYT 433
                                                                                                                                                                            EEMILDFFNSCGYPCPEHSNPFDFYMDLTSVDTQSREREIETYKRVQMLESAFRDSAVCHK
                                                                                                                                                                                                                                                                                          EPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTP
                                                                                        TLENIERTKHLKTLPMIPFKTKDPPGMFCKLGVLLRRVTRNLMRNKQAVIMRLVQNLIMG
                                                                                                                                                                                                                                                                       EPTTGLDCMTANQIVILLAELARRDRIVIVTIHQPRSELFQHFDKIAILTYGEMVFCGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.78;
78.68;
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AAU96988 standard; Protein;
243
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Human ABCG5 mutant R243X protein sequence.

Human; ABCG5; ATP-binding cassette arteriosclerosis; heart disease; hy hypersterolemia; gene 5; sitosterolemia; Alzheimer cholesterol;

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25-SEP-2000; 2000US-235268P
                                                                                                                                   Misc-difference
                                                                                                                                                                                                                         mutant; mutein.
                             2001WO-US29859
                                                                                                                                 Location/Qualifiers 243
                                                                                                                /note= "Wild-type protein truncated
                                                                                                                  at this
                                                                                                                position.
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SERVICES

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RESULT 15
AAB41856
ID AAB41
XX
AC AAB41
XX
O8-FE
XX
DE Human
XX
Human
KW Yulne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC a compound which alters ABCGS activity level comprising contacting a cell CC culture or mammal which have ABCGS to polypeptide with a compound and CC measuring ABCGS biological activity in the cell culture or in mammal, CC where an increase or decrease in ABCGS biological activity compared to CC contacted with the compound, identifies a compound that increases or CC contacted with the compound, identifies a compound that increases or CC decreases ABCGS activity respectively. The cell culture or mammal not CC comprises a mutated ABCGS polypeptide or a wild type polypeptide. The CC ABCGS biological activity, or level of ABCGS minulation of ABCGS activity is useful for treating or preventing CC second cell culture or mammal is also compared with that of a CS stimulation of ABCGS activity is useful for treating or preventing CC disease. The method of the invention is useful for increasing cholesterol acid sequence represents the human ABCGS mutant R243X protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 243
                                                  Human ORFX ORF1620 polypeptide sequence SEQ ID NO:3240
   Human; open reading frame; ORFX; detection;
vulnerary; antipsoriatic; antiparkinsonian;
                                                                                                                                                                   AAB41856 standard;
                                                                                              08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: This sequence is not shown in the specification but is derived from the wild type human ABCG5 protein (AAU96984) given on pages 35-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel mammalian ATP-binding cassette gene 5 polypeptide, and the nucleic acid encoding the polypeptide, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sitosterolemia, arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                              181
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                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Page -; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification
                                                                                                                                                                                                                                                                            RNR 243
                                                                                                                                                                                                                                                                                                                                                      ADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR
                                                                                                                                                                                                                                                                                                                                                                                                              RREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSHV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSC
                                                                                                                                                                                                                                                                                                                       ADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR
                                                                                                                                                                                                                                                                                                                                                                                             RREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                            (first entry)
                                                                                                                                                               Protein; 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABCG5 protein (AAU96984) given on pages 35-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1234; DB 23; Pred. No. 2.1e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and heart diseases
cytostatic; hepatotropic;
nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                          .240
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417 _

KTKDSPGVFSKLGVLLRRVTRNLVRNKLAVÍTRLLQNLIMGLFLLFFVLRVRSNVLKGAI 416 KTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAI

Matches 143; Query Match Best Local

Similarity

21.78;

Score 722; DB 21; Pred. No. 1.1e-67;

Length 144;

Conservative

0;

Mismatches

۲,

0;

Gaps

60

Sequence

144 AA;

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CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, CC which represent the human ORFX open reading frames 1 to 3161. The ORFX CC sequences have activities such as: cytostatic, hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; CC immunostinulant; cardiant; thrombolytic; coagulant; vasotropic; coantidiabetic; hypotensive; dermatological; immunosuppressive; coantiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; coatilityroid; and antianaemic. The sequences can be used for determining CC the presence of or predisposition to, or preventing or treating CC ucleic acids can be used to express ORFX proteins in gene therapy CC vectors. The proteins and nucleic acids may be used to treat cancers, CC ucleic acids can be used to express ORFX proteins in gene therapy CC vectors. The proteins and nucleic acids may be used to treat cancers, CC graft vs host disease, cardiovascular disease, diabetes mellitus, CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, CC allerative disastic anaemia. burns. wounds. bone and cartilace damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                          allergies, aplastic anaemia, burns, wounds, bone and cartilage nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 2444; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus crythematosus; infection;
                                            coagulation; to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticonvulsant; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0127728
2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127607.
99US-0127636.
                                       inhibit thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulant; vasotropic;
                                   and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antidiabetic;
                                                          enhance
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Page 13

Ъ 8 Ω Search completed: June 11, 2003, 09:12:15 Job time: 43 secs 61 QDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSV 120

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OM protein - protein search, using sw model
                                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:

Title: Perfect score: June 11, 2003, 09:04:42 ; Search time 15 Seconds (without alignments) 1800.073 Million cell updates/sec US-09-989-981A-6

1 MGDLSSLTPGGSMGLQVNRG......PALVILGIVVFKIRDHLISR 651

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : "SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	score	Query Match	Length	BG	ID	Description
_ ب	3326	 00	651	- :	ABG5_HUMAN	Q9h222 homo sapien
.		682-3	652	-	ABG5_MOUSE	mus m
. ω		8250	652	-	ABG5_RAT	ratt
4		2410	673	_	ABG8_MOUSE	_
5	697	21.0	673	_	ABG8_HUMAN	
0		20.8	672	۳	ABG8_RAT	
7	676.5	20.3	655	۳	ABG2_HUMAN	
œ	627	18.9	1294	۳	YOH5_YEAST	
وا	. 623	18.7	677	۳	WHIT_LUCCU	_
10	621	18.7	1049	μ	ADP1_YEAST	
11	607.5	18.3	695	۲	WHIT_ANOGA	
12	502.5	18.1	687	_	WHIT_DROME	drosophila
1.3	596.5	17.9	678	_	ABG1:HUMAN	
1 4	591	17.8	679	-	WHIT_CERCA	_
1 1	0.0.0	1.4	1040	- ۱	ABG4_HUMAN	
1 5	5070	17.2	709	٠ 1	WHIT ANOAL	
10	504.U	1.7	000	-	ABG1_MOUSE	
100	74.0	16.9	000	4 بـ	IPC3_CAEEL	
3 5	517 5	15.4	610	۰,	CORT CANTE	
21	454.5	13.7	675	٠,	BROW DROME	
22	435	13.1	899	 -	BROW DROVI	024739 drosophila
23	427	12.8	1499	_	CDR2_CANAL	
24	406.5	12.2	1333	۳	YN99_YEAST	
25	403.5	12.1	1564	_	PDRA_YEAST	
26	399.5		1530	_	BFR1_SCHPO	
27	868	12.0	1501	_	SNQ2_YEAST	
2	392.5	٠	1501	1	CDR3_CANAL	
2 2	165	11.8	1529	_	PDRF_YEAST	
2 0	383.5	11.5	650	۲	ABG3_MOUSE	
۲ د	382	11.5	1501	_	CDR1_CANAL	
מ נג	374	11.0	TICI	- ۱	PDRC_YEAST	Q02785 saccharomyc
į	4	11.6	1171	۲	FURU_1 EAST	P33302 saccharomyc

RA Partel S.B.;
"Two genes that map to the STSL locus cause sitosterolemia: genomic RT." structure and spectrum of mutations involving sterolin-1 and RT sterolin-2, encoded by ABCGS and ABCGB, respectively.";
RL Am. J. Hum. Genet. 69:278-290(2001).
RC -1- FUNCTION: Transporter that appears to play an indispensable role CC in the selective transport of the dietary cholesterol in and out CC of the enteroxytes and in the selective sterol excretion by the

SUBUNIT: May form heterodimers with ABCG8 or be tightly coupled

VARIANT SITOSTEROLEMIA Q-146; H-389; P-419; H-419 AND S-550, AND VARIANT E-604.

MEDLINE-21344600; PubMed=11452359;

Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H., Kojima H., Ose L., Stalenhoefta. Mietinnen T., Bjorkhem I., Bruckert E., Pandya A., Brewer H.B. Jr., Salen G., Dean M., Srivastava A.K.,

45	44	43	42	41	40	39	8	37	36	ω S	34
240.5	241.5	247.5	249.5	250.5	251	254	257	263	263.5	365.5	367
7.2	7.3	7.4	7.5	7.5	7.5	7.6	7.7	7.9	7.9	11.0	11.0
308	355	356	344	231	573	365	365	241	345	1490	1410
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NOSF_PSEST	CYSA_SYNY3	HITC_HAEIN	CYSA_SYNP7	YTRE_BACSU	CYDC_ECOLI	CYSA_SALTY	CYSA_ECOLI	YHBG_HAEIN	ABC_HAEIN	CDR4_CANAL	PDRB_YEAST
								,			
P19844 pseudomonas	~	_	_	034392 bacillus su	٠.	_	P16676 escherichia	P45073 haemophilus	٠.	٠.	P40550 saccharomyc

ALIGNMENTS

OC Euka Mammo OC Euka Mammo OC No No No No No No No No No No No No No	OC Euka OC Euka OC NCBI, RN [1] RN SEQUI RC TISSI RX MEDLI. ACCIONATION ACCIONATION TIONATIONATIONATIONATIONATIONAT		RESULT 1 ABG5_HUMAN ID ABG5_ AC 09422 AC 15-JU DT 15-JU DT 15-JU DT ATP-b GN ABG55
immiration of relative to the control of the contro	Accumulation for the state of t	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606; [1] SEQUENCE FROM N.A., AND VARIANT GLU-604. TISSUE-Liver; MEDLINE=20553648; PubMed=11099417; BETGERKEE, Tian-H.; Graf G.A., Pu L., Grishin N.V.,	HUMAN STANDARD; PRT; 651 AA. AB65.HUMAN STANDARD; PRT; 651 AA. Q9H272; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) ATP-binding cassette, sub-family G, member 5 ABCGS.
E in the regulation of	· · · · · · · · · · · · · · · · · · ·	raniata; Vertebrata; Euteleostomi; atarrhini; Hominidae; Homo. GLU-604. 17; Yu L., Grishin N.V., Schultz J., R., Höbbs H.H.; Percentage Course by porters."; Po	A.) te) 5 (Sterolin-1).

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                                                                           Query Match
Best Local Similarity
Matches 651; Conser
                                                                                                                                                                                                                                      CARBOHYD
                                                                           SEQUENCE
                                                                                                    VARIANT
                                                                                                                         VARIANT
                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam: PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF320293; AAG40003.1; -. EMBL; AF312715; AAG53099.1; -..
                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                             TRANSMEM
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SMART; SM00382; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disease mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00211; ABC_TRANSPORTER; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Strongly expressed in the liver, lower levels in the small intestine and colon.

DISEASE: Defects in ABCG5 are a cause of sitosterolemia, also known as phytosterolemia or shellfish sterolemia, a rare autosomal recessive disorder characterized by increased intestinal absorption of all sterols including cholesterol, plant and shellfish sterols, and decreased bilary excretion of dietary sterols into bile. Sitosterolemia patients have hypercholesterolemia, very high levels of plant sterols in the plasma, and frequently develop tendon and tuberous xanthomas, accelerated atherosclerosis and premature coronary artery disease.

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABCG8 along a pathway regulating diatery-sterol absorption and excretion.
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
TISSUE SPECIFICITY: Strongly expressed in the liver, lower lev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                605459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:13886; ABCG5.
MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSC 60
                                                                          651 AA;
                         Conservative
                                                                                                                         550
                                                                                                                                                419
                                                                                                                                                                                                                                                                                   4443
463
504
525
529
529
                                                                                                                                                                         419
                                                                                                                                                                                                 389
                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG53099.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC_transportr; 1.
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                                                                          72503
                                   100.
                                      .0%;
                                                                           X
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                         0
                        Score 3326;
Pred. No. 1.3
); Mismatches
                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL) 6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                            CYTOPLASMIC
5 (POTENTIAL
                                                                       /FTId-VAR_012249.
950BABFCBB6A1536 CRC64;
                                                                                                                         æ
'∨
                                                                                                                                              /FTId=VAR_012246.
R -> P (IN SITOSTEROLEMIA)
                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                           ATP (POTENTIAL)
                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
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3 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                      /FTId=VAR_012245.
R -> H (IN SITOSTEROLEMIA)
                                                                                                           /FTId-VAR_012248
                                                                                                                                    /FTId=VAR_012247
                                                                                                                                                                                                           FTId-VAR_012244
                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                      Q (IN SITOSTEROLEMIA).
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                                                                                                                       SITOSTEROLEMIA)
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                                     3e-224;
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                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CS7BL/6; TISSUE=Liver;
MEDLINE=20578753; PubMed=11138003;
MEDLINE=20578753; PubMed=11138003;
MEDLINE=20578753; PubMed=11138003;
MEDLINE=20578753; PubMed=11138003;
MEDLINE=20578753; PubMed=11138003;
MEDLINE=20578753; PubMed=1138003;
MEDLINE=2057853; PubMed=2057853; SSUE SPECIFICITY, AND INDUCTION.
MEDLINE-20553648; PubMed-11099417;
Berge K.E., Tian H., Graf G.A., Yu L., G
KWiterovich P., Shan.B., Barnes R., Hobb
"Accumulation of dietary cholesterol in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG5_MOUSE
Q99PE8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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12 (Rel. 41, Last sequence)
12 (Rel. 41, Last annotation)
13 cassette, sub-family
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Rodentia;
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Last annotation updat
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Sciurognathi; Muridae; Murinae; Mus
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                       L., Grishin N.V.,
Hobbs H.H.;
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    sitosterolemia caused
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A.K., Salen
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Best Local :
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InterPro; IPR003439; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutations in adjacent ABC transporters.";
Science 290:1771-1775(2000).
-i- FUNCTION: Transporter that appears to
                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: Upregulated by cholesterol feeding. Possibly mediated by the liver X receptor/retinoic X receptor (LXR/RXR) pathway. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABCG8 along a pathway regulating diatery-sterol excretion (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein TISSUE SPECIFICITY: Expressed in the intestine a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterceytes and in the selective sterol excretion by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: May form heterodimers with ABCG8 or be
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                                                                                                                                                                                     Similarity
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         VADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELA
                                       CROQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRA
                                                                                                                                       MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEP-HSLGILHASYSVSHRVRPWWDITS
                                                                                  COOKWDRQILKDVSLYIESGQIMCILGSSGSGKTTLLDAISGRLRRTGTLEGEVFVNGCE
                                                                                                                            MGELPFLSPEGARGPHINRGSLSSLEQGSVTGTEARHSLGVLHVSYSVSNRVGPWWNIKS
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                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
CYTOPLASMIC
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Pred. No. 1.3
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                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley; TISSUE-Small intestine; MEDLINE-20578753; PubMed-11138003; Sile M. H., Lu K., Hazard S., Yu H., Shulenin S
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15-JUN-2002 (
15-JUN-2002 (
ATP-binding (
                                                                                                                          *Bean-N--Patel S.B.;

"Identification of a gene, ABCG5, important in the regulation of dietary cholesterol absorption.";

Nat. Genet. 27:79-83(2001).

"I FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the liver into bile.

"I SUBUNIT: May form heterodimers with ABCG8 or be tightly coupled the ABCG8 along a pathway regulating diatery-sterol absorption and excretion (By similarity).

"SUBCELLULAR LOCATION: Integral membrane protein (Probable).

"I SUBCELLULAR LOCATION: THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
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Pfam; PF00005; ABC_tran; 1.
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                                  SGLLIGSGFIRNIEEMPIPLKILGYFTFQKYCCEILVVNEFYGLNFTCGGSNTSVPNNPM
                                              AGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNBFYGLNFTCGSSNVSVTTNPM
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2727.5; DB 1; Length 652; Pred. No. 7.7e-183;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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ATP (POTENTIAL).
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RESULT 4
ABG8_MOUS
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                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY, AND INDUCTION.

MEDLINE-20553648; PubMed-11099417;

Berge K.E., Tian H., Graf G.A., Yu L., Grishin N.V., Schultz J

Kwiterovich P., Shan B., Barnes R., Hobbs H.H.;

*Accumulation of dietary cholesterol in sitosterolemia caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                        <del>:</del>
                                                                                                                                                                                                                                                                                                             mutations in adjacent ABC transporters.";
Science 290:1771-1775(2000).
-!- FUNCTION: Transporter that appears to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Two genes that map to the STSL locus cause sitosterolemia: structure and spectrum of mutations involving sterolin-1 and sterolin-2, encoded by ABCG5 and ABCG8, respectively."; am. J. Hum. Genet. 69:278-290(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lu K., Lee M.-H., Hazard S., Brooks-Wilson A., Hidaka H., Ose L., Stalenhoef A.F.H., Mietinnen T., Bjorkhem I., Bruo Pandya A., Brewer H.B. Jr., Salen G., Dean M., Srivastava
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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          ABCG5 along a pathway regulating diatery-sterol absorption and excretion (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein (Probable).

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.

TISSUE SPECIFICITY: Expressed in the intestine and, at lower level, in the liver.

INDUCTION: Upregulated by cholesterol feeding. Possibly mediated by the liver X receptor/retinoide X receptor (LXR/RXR) pathway.

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                         liver into bile.
SUBUNIT: May form heterodimers with
                                                                                                                                                                                                                                                              FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the
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Metazoa; Chordata; C
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Sciurognathi; Muridae; Murinae; Mus
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Pfam; PF00005;
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PROSITE; PS00211; ABC_TRANSPORTER;
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Buropean Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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                               CLMSLIIGFLYYGHGAKQL--SFMDTAALLFMIGALIPFNVILDVYSKCHSERSMLYYEL
                                                     LIMGLFLLFFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQES
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                                                                                                                                                                              Schmitz G., Langmann T., Heimerl S.;
"Role of ABCG1 and other ABCG family members in lipid metabolism.";
J. Lipid Res. 42:1513-1520(2001)
-i-FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the
                                                                                                                                                                                                                                                                                                                       "Two genes that map to the STSL locus cause sitosterolems structure and spectrum of mutations involving sterolin-1 sterolin-2, encoded by ABCGS and ABCGB, respectively."; Am. J. Hum. Genet. 69:278-290(2001).
                                                                                                                                                                                                                                                                             MEDLINE=21474438; PubMed-11590207;
                                                                                                                                                                                                                                                                                                                                                                                        Patel S.B.;
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21344600; PubMed=11452359;
Lu K., Lee M.-H., Hazard S., Brookks-Wilson A., Hidaka H.,
Ose L., Stalenhoef A.F.H., Mietinnen T., Bjozkhem I., Bruc
Pandya A., Brewer H.B. Jr., Salen G., Dean M., Srivastava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), VARIANTS SITOSTEROLEMIA H-184; T-231; Q-263; H-405; P-501; S-543; P-572; E-574; R-574; R-596 AND F-570 DEL, AND VARIANTS H-19; C-54; K-238; V-259; K-400; R-575 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kwiterovich P. Shan B., Barnes R., Hobbs H.H.;
"Accumulation of dietary cholesterol in sitosterolemia
mutations in adjacent ABC transporters.";
Science 290:1771-1775(2000).
                                                                                                                                                                                                                                                                                               REVIEW
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Berge K.E., Tian H., Graf G.A., Yu
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Mammalia; Eutheria;
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L5-JUN-2002
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                    ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and produced by alternative splicing. Isoform 2 is a minu detected in approximately 10% of the cDNA clones. TISSUE SPECIFICITY: Strongly expressed in the liver, in the small intestine and colon. Detectable in a wich
                                                                                SUBCELLULAR LOCATION: Integral membrane protein ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here)
                                                                                                                             SUBUNIT: May form heterodimers with ABCG5 or be tightly co-ABCG5 along a pathway regulating diatery-sterol absorption
                                                                                                                       excretion.
                                                                                                                                                                    liver
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Last annotation update)
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hem I., Bruckert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                known as phytosterolemia or shellfish sterolemia, a rare autosomal recessive disorder characterized by increased intestinal absorption of all sterols including cholesterol, plant and shellfish sterols, and decreased biliary excretion of dietary sterols into bile. Sitosterolemia patients have hypercholesterolemia, very high levels of plant sterols in the plasma, and frequently develop tendon and tuberous xanthomas, accelerated atherosclerosis and premature coronary artery disease. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE) CAUTION: Seems to have a defective ATP-binding region.
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RESULT
          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                         VARSPLIC
                                                                                                                                                                                                                                                                SMART; SM00382; AAA; 1
                                                                                                                                                                                                                                                                       Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                             EMBL; AF351785; AAK84831.1; -
                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (;
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure and spectrum of mutations invosterolin-2, encoded by ABCG5 and ABCG8, Am. J. Hum. Genet. 69:278-290(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley MEDLINE-21344600; Publ
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Ose L., Stalenhoef A.F.H., Mietinnen T., Bjorkhem I., Bruo
Pandya A., Brewer H.B. Jr., Salen G., Dean M., Srivastava
Datol S B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Two genes that map to the STSL locus cause sitosterolemia: structure and spectrum of mutations involving sterolin-1 and sterolin-2, encoded by ABCG5 and ABCG8, respectively.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P58428;
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG8_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L5-JUN-2002
L5-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: May form heterodimers with ABCG5 or be tightly coupled ABCG5 along a pathway regulating diatery-sterol absorption and excretion (By similarity) SUBCELLULAR LOCATION: Integral membrane protein (Probable).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                     produced by alternative splicing. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the
          Similarity
                                                                                                                                                                                                                                                   PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                     IPR003593; AAA_ATPase.
IPR003439; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          into bile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
cassette, sub-family G, member 8 (Sterolin-2).
                                                                                                                                                                                                                                                                                                                                                                                                                               Seems to have a defective ATP-binding region.
                                                                                                                                                                                                                                       Transmembrane;
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Rodentia; Sciurognathi; Muridae;
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       Score
Pred.
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6 (POTENTIAL)
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5 (POTENTIAL
                                                    N-LINKED (GLCNAC. ..)
MISSING (IN ISOFORM 2)
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2 (POTENTIAL).
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        DB 1;
.8e-41;
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                 Length 672;
                                                                 (POTENTIAL).
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; Murinae; Rattus
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Bruckert E
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Allikmets R., Schriml L.M., Hutchinson A., Romano-Spica V., "A human placenta-specific ATP-binding cassette gene (ABCP) chromosome 4q22 that is involved in multidrug resistance."; Cancer Res. 58:5337-5339(1998).
                                                  MEDLINE-99065313; PubMed-9850061;
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Matches
                                                                                                                            ABG2_HUMAN STANDARD; PRT; 655 AA.

Q9UNQO; O95374; Q9NUSO; Q9BY73;

16-OCT-2001 (Rel. 40, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

ATP-binding cassette, sub-family G, member 2

binding cassette transporter) (Breast cancer)

ABCG2 OR ABCP OR BCRP OR BCRP1.
SEQUENCE FROM N.A.
TISSUE-Placenta;
                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                           Homo sapiens (Human)
                                                      NCBI_TaxID-9606
                                                                                                                                                                                                                                                                                                                                                                                             633
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                                                                        Eutheria;
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                                                                        Chordata;
Primates;
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                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                            (Placenta-specific resistance protein)
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                                                                                       Euteleostomi;
                                                                        Homo
                                                                                                                                            protein)
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                                                                                                                                                             ATP-
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Schmitz G., Langmann T., Heimerl S.;

Role of ABCG1 and other ABCG family members in lipid metabolism.";

J. Lipid Res. 42:1513-1520(2001).

-I- FUNCTION: XENOBIOTIC TRANSPORTER THAT APPEARS TO PLAY A MAJOR ROLE
IN THE MULTIDRUG RESISTANCE PHENOTYPE OF A SPECIFIC MCF-7 BREAST
CANCER CELL LINE. WHEN OVEREXPRESSED, THE TRANSFECTED CELLS BECOME
RESISTANT TO MITOXANTRONE, DAUNORUBICIN AND DOXORUBICIN, DISPLAY
DIMINISHED INTRACELLULAR ACCUMULATION OF DAUNORUBICIN, AND
MANIFEST AN ATP-DEPENDENT INCREASE IN THE EFFLUX OF RHODAMINE 123.

-I- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
     ATP-binding; Transmembrane;
DOMAIN 1 395
TRANSMEM 396 416
DOMAIN 417 428
                                                                                                                             Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
SMART; SM00382; AAA; 1.
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between
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                     EMBL; AF103796; AAD09188.1;
EMBL; AF098951; AAC97367.1;
EMBL; AB056867; BAB39212.1;
EMBL; AK002040; BAA92050.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                     Genew; HGNC:74; ABCG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
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                                                                                                   PROSITE; PS00211; ABC_TRANSPORTER; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kage K., Tsukahara
Sugimoto Y.;
                                                                                                                                                                                                    InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
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TISSUE-Breast cancer;
MEDLINE-99080071; PubMed-9861027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breast cancer resistance
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                                                                                                                                 AIQDRVGLLYQFVGATPYTGMLNAVNLFPYLRAVSDQESQDGLYQKWQMMLAYAL-HYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                     TLIMTICFVFMM;FSGLLVNLTTIASWLSWLQVFSIPRYGFTALQHNEFLGQNFCPG---
  LNATGNNPCNYA----
                   VSVTTNPMCAFTQGIQFIEKTCPG
                                                        VALLSTAGV--LVGSGFLRNIQEMPIPFKIISYFTFQKYCSETLVVNEFYGLNFTCGSSN 591
                                                                            MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLM:--MVAYSASSMALAIAAGQSVVSVA
                                                                                               FSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSV
                                                                                                                                                                                                                                          FKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIINGDSTAVALNR
                                                                                                                                                                                                                                                            FQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQ----SK
                                                                                                                                                                                                                                                                                                                                                                                                                           SQSSLEGAPATAP---EPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVE
                                                                                                                    GIQNRAGVLF-FLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP
                                                                                                                                                           TT----SFCHQLRWYSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDST----
                                                                                                                                                                              KTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFL--LFFVLRVRSNVLKG
                                                                                                                                                                                            EEDFKATEIIEPSKODKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKKITVFKEISY
                                                                                                                                                                                                                      ERE----IETSKR-----VQMIESAYKKSAICHKT-----LKNIERMKHLKTLPMVPF
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N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
V -> A (IN REF. 2 AND 4)
E -> Q (IN REF. 2 AND 4)
E -> S (IN REF. 1).
-TCTG
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Pred. No. 9.8e-40;
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ATP (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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2 AND 4).
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(POTENTIAL).
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RESULT 8
YOH5_YEAST
YOH5_YEAST

STANDARD;

PRT;

1294 AA.

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Matches 181
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SMART; SM00382; AAA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tzermia M., Katsoulou C., Alexandraki D., Sequence analysis of a 33.2 kb segment f chromosome XV reveals eight known genes a
                                                                                                                                                                                                 CARBOHYD
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Yeast 13:583-589(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0005435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of a 33.2 kb segment from the left arm of yeast chromosome XV reveals eight known genes and ten new open reading frames including homologues of ABC transporters, inositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, C
16-OCT-2001 (Rel. 40, I
16-OCT-2001 (Rel. 40, I
Probable ATP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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MEDLINE-97321807; PubMed-9178509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales;
NCBI_TaxID=4932;
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Q1-NOV-1997 (Re
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                                                                   65
                                                                                                 Similarity
            VSELMEKNVCSYVSQDDDHLLAALTVKETLKYAAALRLHHLTEAERMERTDNLIRSLGLK
                                         TKEILQSVNAIFKPGMINAIMGPSGSGKSSLLNLISGRL-KSSVFAKFDTSGSIMFNDIQ
                                                             TRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFL----GEVYVNGRA
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Last annotation update)
t transporter YOL074C/YOL075C.
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                                                                                     Score 627; DB
Pred. No. 6.7e
06; Mismatches
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    Transmembrane;

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5.7e-36;
hes 228;
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Q05360;
Q1-FEB-1995
Q1-NOV-1997
16-OCT-2001
                                                        Elizur A., Vacek A.T., Howells A.J.;

"Cloning and characterization of the white and topaz eye color genes from the sheep blowfly Lucilia cuprina.";

J. Mol. Evol. 30:347-358(1990).

-I- FUNCTION: MAY BE PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY FOR THE TRANSPORT OF PIGMENT PRECURSORS INTO PIGMENT CELLS RESPONSIBLE FOR EYE COLOR.

-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                        Garcia R.L., Perkins H.D., Howells A.J.;
"The structure, sequence and developmental pattern
the white gene in the blowfly Lucilia cuprina.";
Insect Mol. Biol. 5:251-260(1996).
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-97087158; PubMed-8933176;
                                                                                                                                                          MEDLINE-90264941; PubMed-1971656;
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1224 FAFPGNLKLTCEDGGKNSDGT----CEFANG 1250
                                             NEFYG-LNFTC--GSSNVSVTTNPMCAFTQG
                                                                                                                                                                                    PFFLAYMTLELPLSALASVLYAVFTVLACGL-PRTA--GNFFATVYCSFIVTCCGERLGI 1167
                                                                                                                                                                                                                                    QMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLI---
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                                                                                               MTNTFFERPGFVVNCISIILSIGTQMSGLMSL---
                                                                                                                                       VLLGIVQNPN-IVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVV
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pai Insecta; Pterygota; Neoptera; Endopterygota; Dig Muscomorpha; Oestroidea; Calliphoridae; Lucilia. NCBI_TaxID=7375; Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly). Eukaryota: Metazoa: Arthropoda: Mandibulata: Pancrustacea; He STANDARD; Last sequence update)
Last annotation updat Created) PRT; 677 update) ⋧ Diptera; Brachycera; Hexapoda;

SEQUENCE OF 490-584 FROM N.A.

of.

expression

of

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                                                                                             AALLAPHLIGEFLT----LVLLGIVONPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFK
                                                                                                                                                 VLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFS
                                                                                                                                                                                      AVITRLLQNLIMGLEL-LEFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFP
                                                                                                                                                                                                                                                                 TPVEAVDFFSFIGAQCPTNYNPADFYVQVLAV----VPGREIESRDRISKICDNFAVGKVS
                                                                                                                                                                                                                                                                                      TPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAIC
                                                                                                                                                                                                                                                                                                             CDEPTSGLDSFMAASVVQVLKKLSQRGKTVILTIHQPSSELFELFDKILLMAEGRVAFLG
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ATP-binding; Transmembrane; Transpor
ATP (POTENTIAL).
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                ATSRFTMNFLILYSFIPALVILGIVVFKIRDHLISR
                                    WLSYFSWFRYANEGLLINGWADVQPGEITCTSTNT----
                                                            IISYFTFQKYCSEILVVNEFYGL---NFTCGSSNVSVTTNPMCAFTQGIQFIEKTCP--G
                                                                                                                             SELPVFMRETRSRLYRCDTYFLGKTLAELPLELVVPFLFIAIAYPMIGLRPGIT---HFL
                                                                                                                                                                          LVKVRLIQTTMVAVLIGLIFLNQPMTQV----GVMNINGAIFLFLTNMTFQNVFAVINVFT
                                                                                                                                                                                                                      REMEQNFQK-----IAAKTDGLQKDDETTILYKASWFTQFRAIMWRSWISTLKEPL
                                                                                                                                                                                                                                           HKTLKNIERMKHLKTLPMVPFKT----KDSPGV-----FSKLGVLLRRVTRNLVRNKL
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                                                                                  SALALVTLVANVSTSFGYLISCASTSTSMALSVGPPLTIPFLLFGGVFL-NSGSVPVYFK
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TIGR00955;
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IPR005284; Pigment_permease.
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Score 623; DB
Pred. No. 5.5e
44; Mismatches
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                                       TCPSSG
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ADP1_YEAST
    CARBOHYD
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P25371;
01-MAY-1992
                                                                                                                            TRANSMEM
CARBOHYD
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MEDILINE-92327849; PubMed-1626432;

Skala J., Purnelle B., Goffeau A.;

Skala J., Purnelle B., Goffeau A.;

"The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of chromosome III from Saccharomyces cerevisiae reveals seven open reading frames including the RVS161, ADP1 and PGK genes.";

Yeast 8:409-417(1992).
                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purnelle B., Skala J., Goffeau A.; "The product of the YCR105 gene located on th Saccharomyces cerevisiae presents homologies
                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X59720; CAA42328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable ATP-dependent permease pred
ADP1 OR YCR011C OR YCR105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                 NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00382;
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                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00211; ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92160395; PubMed=1789009;
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$40914; $40914.
$0000604; ADP1.
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878
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1001
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    430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        license agreement
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  N-LINKED
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                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
PROBABLE ATP-DEPENDENT PERMEASE
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RESULT 11
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ID WHIT_A
AC Q27256
DT 01-NOV
DT 16-OCT
DE White
GN W.
OS Anophe
OC Eukary
OC Insectoo
CCUlico
OX NCBL_T
RN [1]
RP SEQUEN
RC STRAIN
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Q27256; Q17006;
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                             Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Anopheles.
           SEQUENCE FROM N.A. STRAIN-Suakoko / G3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                    White protein.
                                                    NCBI_TaxID=7165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 IIGFVDQDDFLLPTLTVFETVLNSALLRLPKAL--SFEAKKARVYKVLEELRIIDIKDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VVQNLVFDIKILALFNVVFLIMGYL
                                                                                                                                                                                                                                                                                       LILYSFIPALVILGI--VVFKIRDHL
                                                                                                                                                                                                                                                                                                                                                             ILVVNEF - -
                                                                                                                                                                                                                                                                                                                                                                                 ILTIGIIFEDLNNSIILSVLVLL---GSLLESGLFINTKNITNVAFKYLKNESVFYYAYE
                                                                                                                                                                                                                                                                                                                                                                                                 LVLLGIV---QNPNIVNSVVALLSIAGVLVGSGFLRNIQEMP-IPFKIISYFTFQKYCSE:::||: | : : : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                      --LAYYISKIMSEVVPLRVVPPILLSLIVYPMTGLNMKDNAF-FKCIGILILFNLGISLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMLAYAL----HVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NV-SNDISG-FQNRMGLFFFILTYFGFVTFTGL----SSFALERIIFIKERSNNYYSP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVRSNVLKGAIQDRVGLLY---QFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDLPT-----GQQSAGFLQQLSILNSRSFKNMYRNPKLLLGNYLLTILLSLFLGTLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KHLKTLPMVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLVLSIHQPRSNIFYLFDKLVLLSKGENYYSGNAKKVSEFLRNEGYICPDNYNIADYLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITFEAGPQGKRRRIRNISDLEAGTDTNDIDNTIHQTTFTSSDGTTQREWAHLAAHRDEIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGNYSLGGISTGERRRYSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR-RNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKK---VEAVMAELSLSHVADRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLNEISGIVKPGQILAIMGGSGAGKTTLLDILAMK-RKTGHVSGSIKVNGISMDRKSFSK
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1049
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35, Last sequence update)
40, Last annotation updat
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117231 MW; ABC9CE54BCFDF6A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 621; DB 1; Pred. No. 1.3e-35;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGR00955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U29485; AAC46994.1; EMBL; U29484; AAC47423.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of the white gene from Anopheles gambiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIB_AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003439; ABC_transportr.
InterPro; IPR005284; Pigment_permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U29486; AAC46995.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insect Mol. B101. 4:217-231(1995).
-!- FUNCTION: MAY BE PART OF A MEMBRANE-SPANNING PERMINERSPORT FOR THE TRANSPORT OF PIGMENT PRECURSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collins F.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Besansky N.J., Bedell J.A., Benedict M.Q., Mukabayire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96423158; PubMed=8825759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELLS RESPONSIBLE FOR EYE COLOR.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
        392
                                  344
                                                             335
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                                                                                                                                                                                   FSQLGIPCPPNYNPADFYVQMLAI---APAKEAECRDMIKKICDSFAVSPIAREVLETAS
                                                                               FNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIE
                                                                                                            DSFNAHSVLQVLKGNAMKGKTIILTIHQPSSELYCLFDKILLVAEGRVAFLGSPYQSAEF
                                                                                                                            DCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDF | : :: | : | : | : | : : | : | : : |
                                                                                                                                                                    QHRVQEVLQELSLVKCADTIIGAPGRIKGLSGGERKRLAFASETLTDPHLLLCDEPTSGL
                                                                                                                                                                                                                         KISPNAVRALNGVPVNAEQLRARCAYVQQDDLFIPSLTTREHLLFQAMLRMGRDVPASVK
                                                                                                                                                                                                                                     FLGEVYV---NGRALREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSF-
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                               RMKHLKTLPMVPFKTKDSPGVFSKL-GV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00211; ABC_TRANSPORTER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003593; AAA_ATPase.
IPR003439; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                      Conservative 124;
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77218 MW;
·VAGKGMDEPYMLQQVEGVGSTGYRSSWWTQFYCILWRSWLSVLKDPMLVK
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ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                    Score 607.5; DB 1;
Pred. No. 6.9e-35;
4; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N -> S (IN REF. 1; AAC47423).
SRS -> YAR (IN REF. 1; AAC47423).
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., I P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandra'. D., Bolshakov S.,
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A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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A Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-85134865; PubMed-6084717;

O'Hare K., Murphy C., Levis R., R

DNA sequence of the white locus
J. Mol. Biol. 180:437-455(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHIT_DROME STANDARD; PRT; 687 AA. P10090; Q9V3A2; Q9XY33; Q1-MAR-1989 (Rel. 10, Created) Q1-MOV-1991 (Rel. 20, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pepling M., Mount S.M.; "Sequence of a cDNA from the Drosophila melanogaster white gene."; Nucleic Acids Res. 18:1633-1633(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White protein.
W OR EG:BACN33B1.1 OR CG2759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90221897; PubMed-2109311; Pepling M., Mount S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Dual-tagging gene trap of novel genes Genetics 157:727-742(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto D.;
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PIR;

S07263; FYFFW. S08635; S08635

FBgn0003996; w.

IPR003593; AAA_ATPase.
IPR003439; ABC_transportr

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AA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
AA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
AA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
AA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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AA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
AA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.L.,
AA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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AA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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AA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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AA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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AA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
AA Walliams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
AA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
AA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
AA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
AA The Genome Sequence of Drosophila melanogaster.*;

The Genome Sequence of Drosophila melanogaster.*;
                                                                                                  EMBL; X51749; CAA36038.1; -. EMBL; X02974; CAA26716.1; -. EMBL; AB028139; BAA78210.1; -. EMBL; AB003425; AAP45826.1; -. EMBL; AL133506; CAB65847.1; -. EMBL; X76202; CAA53795.1; -.
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Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Benos P.V., Gatt M.K., Ashburner M., Demailles J., Cadieu I
Benos P.V., Gatt M.K., Mortier S., Galiet S., Golows S., Kadueno S., Gloux S., Louis C., Siden-Kiamos I., Bolshakov S.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
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McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics 122:595-606(1989).
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                                                                                                                                                                                                                                                                                                                                                                        between
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SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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an email to license@isb-sib.ch).
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39145; PubMed=2503416;
, Belote J.M., McKeown
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                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: Integral membrane protein.
BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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X., Smith H.O.,
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Pfam; PF00005; ABC_
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                            CLPLDYVGLAIL-IVSFRVLAYLALR
                                                                                  TSFGYLISCASSSTSMALSVGPPVIIPFLLFGGFFLNSGSVPVYLKWLSYLSWFRYANEG
                                                                                                                            VLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIV
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                                           FIP----ALVILGIVVFKIRDHLISR
                                                                     LVVNEFYGL---NFTCGSSNVSVTTNPMCAFTQGIQFIEKTCP--GATSRFTMNFLILYS
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ATP-binding; Transmembrane; Transport.
130 137 ATP (BY SIMILARITY).
                                                         LLINQWADVEPGEISCTSSNT--
                                                                                                                ELPLFLTVPLVFTAIAYPMIGLRAGVLHF-----
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TIGR00955;
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485
533
563
578
678
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                                                                                                                                                                                   -GVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFL-LFFVLRVRSN
                                                                                                                                                                                                                                                                                                                                                                           75672 MW;
                                                                                            -----VLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEI
                                                                                                                                                                                                                                                                                                                                                      18.1%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3a01204; 1.
                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                VGAQCPTNYNPADFYYQVLAVVPGREIESRDRIAKIC -> ITLHLNSYPAWVPSVLPTTIRRTFTYRCWPLCPDGRSSPVI GSPRYG (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                    GDSGA -> LIFEIPYHCRVTAD (IN
                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                          24AFAD799DE0D396 CRC64;
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                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                            602.5;
                             680
                                          651
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                                                       TCPSSGKVILETLNFSA--A
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                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                              -FNCLALVTLV--ANVS
                                                                                                                                                                                                                                                                                                                                                           687;
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                                                                                                                                                                                                                                                                                                                               123
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RESULT 13
ABG1_HUMAN

Wu R.; mammalian

homolog

of

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XX MEDLINE-20289799; PubMed-10830953;
A Hattori M., Fujlyama A., Taylor T.D., Watanabe H., Yada T.,
A Hattori M., Fujlyama A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Chi M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Menzel U., Delabar J., Schillabel M., Schudy A., Simmermann W.,
A Rosenthal A., Kudoh J., Schilhabel M., Schudy A., Simmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Minoshima S., Schoen O., Desario A., Relchelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Relchelt J., Kauer G., Bloecker H.,
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
A Rehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
A Hehrach H., Relnhardt R., Yaspo M.-L.;
The DNA sequence of human chromosome 21.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG1_HUMAN STANDARD; PRT; 678 AA.
P45844; Q9BXL0; Q9BXL1; Q9BXL2; Q9BXL3; Q9BXL3; Q9BXK8,
Q9BXK8, Q9BXK9; O1-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP-binding cassette, sub-family G, member 1
(ATP-binding cassette transporter 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE-2040883; PubMed-10950923;
Berry A., Scott H.S., Kudoh J., Tallor I., Korostishevsky M.,
Wattenhofer M., Guipponi M., Barras C., Rossier C., Shibuya K.,
Wang J., Kawasaki K., Asakawa S., Minoshima S., Shimizu N.,
Antonarakis S.E., Bonne-Tamir B.;
"Refined localization of autosomal recessive nonsyndromic deafness
DFNB10 locus using 34 novel microsatellite markers, genomic
structure, and exclusion of six known genes in the region.";
Genomics 68:22-29(2000).
Croop J.M., Tiller G.E., Fletcher J.A., Goldenson D., Arciniegas S., Son D., Wu "Isolation and characterization of a ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porsch-Oezcueruemez M., Langmann T., Helmerl S., Borsukova H., Kaminski W.E., Drobnik W., Honer C., Schunacher C., Schmitz G.; "The zinc finger protein 202 (ZMF202) is a transcriptional repressor of ATP binding cassette transporter Al (ABCA1) and ABCG1 gene expression and a modulator of cellular lipid efflux."; J. Biol. Chem. 276:12427-12433(2001).
                                                                                                   TISSUE-Fetal brain;
MEDLINE-97186700; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene and mapping to Am. J. Hum. Genet.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 2; 3; MEDLINE-21092576; PubMed-11162488;
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Eukaryota; Metazoa; (
Mammalia; Eutheria; 
                                                                                                                                                                        SEQUENCE OF 33-678
                                                                                                                                                                                                                                                                                                    Lorkowski S., Rust S., Engel
Assmann G., Cullen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-21192304; PubMed-11279031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 405:311-319(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96256850; PubMed=8659545;
Chen H.M., Rossier C., Lalioti M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perrin G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 3-678 FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÀBCG1 OR ABC8 OR WHT1.
                                                                                                                                                                                                                                  sequence and structure Biophys. Res. Commun. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antonarakis S.E.
                                                                                                       PubMed=9034316;
                                                                                                                                                                     FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
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Catarrhini;
                                                                                                                                                                                                                            of the human ABCG1 (ABC8) gene."; 280:121-131(2001).
                                                                                                                                                                                                                                                                                                                               Jung
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                                                             M.L.,
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                                                                 Raab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxysterols."
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MEDLINE=20105556; PubMed=1063916;
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Gene 185:77-85(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membranes.

ALTERNATIVE PRODUCTS: At least 7 isoforms; 1 (sho 3/ABDE, 4/G, 5/F, 6/HI and 7/C; are produced by a splicing and alternative initiation.

TISSUE SPECIFICITY: EXPRESSED IN SEVERAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver X receptor/ret
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: Strongly induced in monocyte-derived macrophages during cholesterol influx. Conversely, mRNA and protein expression are suppressed by lipid efflux. Induction is mediated by the liver X receptor/retinoide X receptor (LXR/RXR) pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the ABCG subfamily.
SUBCELLULAR LOCATION: Integral membrane protein.
Predominantly localized in the intracellular com
associated with the endoplasmic reticulum (ER) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FÜNCTION: Transporter involved in macrophage lipid homeostasis. It an active component of the macrophage lipid export complex. Could also be involved in intracellular lipid transport processes. The role in cellular lipid hemeostasis may not be limited to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBFAMILY.
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                                                                                                                                      AJ289145;
AJ289146;
                                                                                                                                                                                                                                                                                                                                                                                                      AJ289137;
AJ289138;
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AB038161;
                                                                                                                                                                                                                                                                                                                                                                          AJ289139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X91249; CAA62631.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Res. 42:1513-1520(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May form heterodimers with several heterologous partners
                                                                                                                                      CAC00730.
CAC00730.
CAC00730.
                                                                                                                                                                                                                                    CAC00730.
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CAC00730.1;
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Q17320;
Q1-NOV-1997
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                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                       Zwiebel L.J., Saccone G., Zacharopoulou A., Besansky N.J., Favia G., Collins F.H., Louis C., Kafatos F.C.;
"The white gene of Ceratitis capitata: a phenotypic marker for germline transformation.";
Science 270:2005-2007(1995).
-- FUNCTION: MAY BE PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY FOR THE TRANSPORT OF PIGMENT PRECURSORS INTO PIGMENT CELLS RESPONSIBLE FOR EYE COLOR.
-- SINILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFANILY.
                   InterPro; IPR003439; ABC_transportr.
InterPro; IPR005284; Pigment_permease.
Pfam; PF00005; ABC_tran; 1.
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Tephritoidea; Tephritidae; Ceratitis.
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQK--KVEAVMAELSLSHVA
FIGLALLIVG---FRISAYI
                              FIP-ALVILGIVVFKIRDHL
                                                                                         NEFYGL---NFTCGSSNVSVTTNPMCAFTQGIQFIEKTCP--GATSRFTMNFL---ILYS
                                                                                                                                                               VALLS----
                                                                                                                                                                                                                     FSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSV
                                                                                                                                                                                                                                                                                     GAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTLIGVPGRVKGLSGGERKRLAFASEALTDPPLLICDEPTSGLDSFMAHSVVQVLKKLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEV--YVNGRALRRE
                                                               NOWADVKPGEITCTLSNT--
                                                                                                                                                                                         LFLVVPFLFTAIAYPLTGLRPGVDHF------FTALALVTLV--ANVSTSF
                                                                                                                                                                                                                                                       -GVMNINGAIFLELTNMTFQNSFATITVFTTELPVFMRETRSRLYRCDTYFLGKTIAELP
                                                                                                                                                                                                                                                                                                                     ENEYTYKASWFMQFRAVLWRSWLSVLKEPLLVKVRLLQTTMVAVLIGLIFLGQQLTQV--
                                                                                                                                                                                                                                                                                                                                                     -----SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFL-LFFVLRVRSNVLK
                                                                                                                                                                                                                                                                                                                                                                                     YVQVLAV---VPGREVESRDRVAKICDNFAVGKVSREMEQNFQ-----KLVKSNGFGKED
                                                                                                                                                                                                                                                                                                                                                                                                                     YMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGKTVILTIHOPSSELFELFDKILLMAEGRVAFLGTPGEAVDFFSYIGATCPTNYTPADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMQARCAYVQQDDLFIGSLTAREHLIFQAMVRMPR-HMTQKQKVQRVDQVIQDLSLGKCQ
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477
525
555
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28.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 591; p. 34; pred. No. 9.4e-34; ches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
; 3F9CBC78A835C4CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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669
                              648
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                                                                                                                                                          IAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transport
                                                            -TCPSSGEVILETLNFSASDLPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 15
ABG4_HUMAN

ID ABG4_HUMAN

ID ABG4_HUMAN

ID ABG4_HUMAN

STANDARD; PRT; 646 AA.

AC Q9H172;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last snotation update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE AFP-binding cassette, sub-family G, member 4.

GN ABCG4 OR WHITE2.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
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Best Local Sim
Matches 171;
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CARBOHYD
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Oldfield S., Lowry C.A., Lightman S.L.;
"Cloning and expression of a novel mammalian white family
BABC-transporter: WHITE2.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in macrophage lipid homeostasis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:13884; ABCG4.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003339; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monocyte-derived macrophages.";
Biochem. Biophys. Res. Commun. 288:483-488(2001):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ300465; CAC17140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 20-646 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21518231; PubMed-11606068; Engel T., Lorkowski S., Lueken A., Rust S., Schlueter B., Berger G., Cullen P., Assmann G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fam; PF00005:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSITE; PS00211; ABC_TRANSPORTER; 1.
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207 LLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAIL 266
                                                             167 NLKLSEKQ----EVKKELVTEILTALGLMSCSHTRTAL-----LSGGQRKRLAIALE
                                                                                                                                  153 LLAIRRGNPGSFQKKYEAV-----MAELSLSHVADRLIGNYSLGGISTGERRRVSIAAQ 206
                                                                                                                                                                                                       109 STFMNILAGY--RESGMKGQILVNGRPRELRTFRKMSCYIMQDDMLLPHLTVLEAMMVSA
                                                                                                                                                                                                                                                                         93 TTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTA 152
                                                                                                                                                                                                                                                                                                                                                 54 PKRSAVDIEFVELSYSVREGPCW-----RKRGYKTLLKCLSGKFCRRELIGIMGPSGAGK
                                                                                                                                                                                                                                                                                                                                                                                                               33 PEPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSSGSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 646 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Transmembrane; Transport.

1 393 CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.48;
27.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 578.5; DB 1; Length 646;
Pred. No. 6.6e-33;
6; Mismatches 274; Indels 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
9CCEC6E150772611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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	616 ATSRFTMNFLILYSFIPALVILGIVVFKIR 645 :: : : : : : 612 EDAKLYMDFLVLGIFFLALRLLAYLVLRYR 641	Оy	пρ
611	559 FKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCFG 615 : ::	ОУ	n 0
55E	499 FGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIP 558	Qy Db	пΩ
498 502	439 VNLEPVLRAVSDQESQDGLYQKWQMMLAYALHVLPESVVATMIFSSVCYWTLGLHPEVAR 498	Qy	п о
442	379 LVRNKLAVITRLLQNLIMGLELLEFVLRVRSNVLKGAIQDRVGLLYQFVGATDYTGNLNA 438 	Ф	п о
378 384	327 SAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKDSPGVFSKLGVLLRRVTRN 370	Qy Qy	п с
32 325	267 SFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRVQMIE 320	Qy Db	п О
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Search completed: June 11, 2003, 09:12:37 Job time: 18 secs

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Maximum Match 100%
Listing first 45 summaries
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

QY 313 EREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLDMVPF 356	GMELITDPSILFLDEPTTGLDSSTANAVLLLLL ALLSFGELIFCGTPAEMLDFENDCGYPCPEHSN : : :: TLLASGRLMFHGPAQEALGYFESAGYHCEAYNN	QY 138 LLSSLTVRETLHYTALLAIRRGNPG-SFQKKVEAVMAELSLSHVADRLIGNYSLGGISTG 196 ::: :: :: : :	Qy 21 SQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSCROQWTRQILKDVSLYVE 77	Query Match 20.5%; Score 682.5; DB 4; Length 655; Best Local Similarity 29.2%; Pred. No. 1.9e-64; Matches 182; Conservative 138; Mismatches 249; Indels 55; Gaps 18;	RESULT 1 US-09-245-808-1 Sequence 1, Application US/09245808 Patent No. 6313277 GENERAL INFORMATION: APPLICANT: Doyle, L. Austin APPLICANT: Doyle, L. Austin APPLICANT: ADVICES. TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which TITLE OF INVENTION: BREAST ON ON ON ON ON ON ON ON ON ON ON ON ON	

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PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3731
LENGTH: 248
TYPE: PAT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3731
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                                                                Sequence 2, Applicati
Patent No. 5994088
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                      190 DEGMTMVIVTHEMRFAK-EVSNQIAFIHEGVIAEQGTPE---DIFN---HPKTEELQRF 241
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                                                                                                                                                                                                                                                                                                                                                                                                               ----QFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSH 179
                                                                                                      Application US/08752447
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29.3%; Pred. No. 8.4e-18;
ive 53; Mismatches 92
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Best Local Similarity
Matches 153; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILLING CALLED ATTORNEY/AGENT INFORMATION:
NAME: No. 5994088nan, Kevin
NAME: No. 5994088nan, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,447
FILING DATE: 15-NOV-1996
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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STATE: Illinois
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                                                                                             FLQGFTFGKAGEILTKRLRYMVFRSMLRQDVSWFHDPKNTTGALTTRLANDAAQVKGAIG 830
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300 South Wacker Drive, Seventh Floor
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                                                     GLLYQFVGATPYTGMLNAVNLFPVL---
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Pred. No. 1.5e-16;
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Length 1280; Indels 250;

Gaps

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490

RAVSDQE 452

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271 549

320

OY 101 GRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRR 158	41 397	Query Match 7.3%; Score 244; DB 4; Length 1280; Best Local Similarity 20.7%; Pred. No. 1.5e-16; Matches 153; Conservative 106; Mismatches 229; Indels 250; Gaps 32;	: INFORMATION FOR SEQ ID NO: 2: : SEQUENCE CHARACTERISTICS: : LENGTH: 1280 amino acids : TYPE: amino acid : TOPOLOGY: linear : MOLECULE TYPE: protein US-09-316-167-2	NAME: NO. 6365357nan, Revin E REGISTRATION NUMBER: 35,303 REFERENCE/DOCKET NUMBER: 95,1121 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001	FILING DATE: 05/09/310,16/ FILING DATE: 05/09/310,16/ CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/752,447 FILING DATE: 15-NOV-1996 ATTORNEY/ACENT INFORMATION.	A R R S	ZIP: 60666 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	II II II II II	ENTION: Methods and Reagents ENTION: Using Immunoligaal Ac QUENCES: 2 CE ADDRESS:	INFORMATION: INFORMATION: CANT: Mechetner, Eugene CANT: Roninson, Igor B		1039 EVVENYPTRPDIPVLOGL	un vo i		453 SQDGL- 889 ELEGAG
; FILING DATE: 05/00//04/04/04/04/04/04/04/04/04/04/04/04	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/OB/704 6405	USA)25 ;ADABLE F(;PE: F10	Co mmoxx	6492 40. S INICANII	Qy 589 SSNVSVTTNPMCAFTQGI 606 Db 1039 EVVENYPTRPDIPVLQGL 1056 RESULT 5	Qy 534VALLSIAGVLVGSGFLRNIQEMPIPEKIISYPTEQKYCSEILVVNEPYGLNFTCG 588	Qy 481 IFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEPLTLVLLGIVQNPNIVNSV 533	Qy 453 SQDGLYQKWQMMLAYALHVLPESVVATM 480	Qy 418 DRVGLLYQFVGATPYTGMLNAVNLEPVLRAVSDQE 452	QY 390 LLQNLIMGLELLEFVLRVRSNVLKGAIQ 417	Qy 364VFSK-LGVLLRRVTRNLVRNKLAVITR 389 III	Qy 321RVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKDSPG 363	272 IFCGTPAEMLE : :: :: :: :: :: :: ::	Oy 212 KVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGEL 271 :: : : : :	OY 159 GNPGSFOKKVEAVMABLSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDP 211

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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1279 amino acids
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
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nes 152; Conserv
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STRANDEDNESS: si
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                                                                                 1040 VFNYPTRPDIPVLQGL 1055
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                                                                                                                     NVSVTTNPMCAFTQGI 606
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Best Local Similarity 20.7%;
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Patent No. 5
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APPLICATION NUMBER: US
FILING DATE: 05-JAN-19
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch diskette
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OPERATING SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/8 FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/3 FILING DATE: 31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 07068
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                                                                                                                                                  607
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                                                                                                                                                                                                                                                                                         491 GRONVIMDEIEKAVKEANAYDFIMKLPHKFDTLYGERG-AQLSGGQKQRIAIARALVRNP
                                                                                                            324 MIESAYKKSAICHKTLKNIERMKHL----
                                                                                                                                                                                                                                             212 KVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGEL
                                                                                                                                                                                                                                                                                                                                                                                                 101 GRIGRAGTFIGEVYVNGRALR--REQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                         397 VHFSYPSRKEVK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 LHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMS
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VGVFCAIINGGLQPAFAIIFSKIIGVFTRIDDPETKRQNSNLFSLLFLALGIISFITFFL 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                            IFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETS-----KRVQ
                                                                                                                                                                                                                KILLLDEATSALD-TESEAVVQVALDKARKGRTTIVIAH--RLSTVRNADVIAGFDDGVI
                                                                    MSSNDSRSSLIRKRSTRRSVRGSQAQDRKLSTKEALDESIPPVSFWRIMKLNLTEWPYFV 712
                                                                                                                                                  VERGNHDELM----
                                                                                                                                                                                                                                                                                                                           GNPGSFQKKVEAVMAE------LSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDP 211
                                                                                                                                                                                                                                                                                                                                                               -RL--YDPTEGMYSYDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRY------
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Cecchi & Stewart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPROVED EXPRESSION OF HUMAN
MULTIDRUG RESISTANCE GENES AND IMPROVED
SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS
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                                    -VFSK-LGVLLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 240; DB 2
Pred. No. 4e-16;
                                                                                                                                            -- KEKGIYFKLVTMQTAGNEVELENAADESKSEIDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 230; Indels 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                          ----KTLPMVPF-----KTKDSPG--
                                -RVTRN-----LVRNKLAVITRLL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1280;
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Gaps

32;

441

490

Qy 212 KVMLFDEPTTGLDCMTANOIVVLLVELARRNIVVLTIHQPRSELFQLFDKIAILSFGEL 271	Query Match Best Local Similarity 20.7%; Pred. No. 4e-16; Matches 152; Conservative 108; Mismatches 230; Indels 246; Gaps 32; Qy 41 LHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMS 100	RESULT 7 \$206352-4 \$206352-4 \$PAtent No. 5206352 ; APPLICANT: RONINSON, IGOR B.; PASTAN ITA H.; GOTTESMAN, ;MICHAEL M. **TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA ;SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS **NUMBER OF SEQUENCES: 4 **CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/622,836 **FILING DATE: 24-SEP-1990 **PRIOR APPLICATION NUMBER: 892,575 **FILING DATE: 01-AUG-1986 **APPLICATION NUMBER: 845,610 **FILING DATE: 28-MAR-1986 **SEQ ID NO:4: LENGTH: 1280	Qy 392 QNLIMG
REGISTRATION UNMBER: 37,315 REFERENCE/DOCKET NUMBER: 1G5-9.1 TELECOMMUNICATION INFORMATION: TELEPHONE: (508) 872-8400 TELEPAX: (508) 872-5415 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LERNCTH: 1684 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein	RESSEE: G EET: Onlor TE: Massa MTRY: Uni: 01701 01701 TER READAB IUM TYPE: FUTER: PA IUM TYPE: FUTER: PA IUM TYPE: FUTER: PA IUM TYPE: FATING SIS TWARE: PA IUCATION N LICATION	Qy 591 NVSVTTNPMCAFTQGI 606 Db 1041 VFNVPTRPDIPVLQGI 1056 RESULT 8 US-08-665-259-25 Sequence 25, Application US/08665259 Patent NO. 6028173 GENERAL INFORMATION: Timothy C. APPLICANT: Landes, Gregory M. APPLICANT: Connors, Timothy D. APPLICANT: Dackowski, William R. APPLICANT: Van Raay, Terence J. APPLICANT: Van Raay, Terence J. APPLICANT: Van Raay, Terence J. APPLICANT: Van Raay, Terence J. APPLICANT: NOVEL HUMAN CHROMOSOME 16 GENES, TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME CORRESPONDENCE ADDRESS:	Oy 364

US-08-665-259-25

Matches

78;

Conservative

43;

Score 239.5; DB 3; Pred. No. 7.3e-16; 3; Mismatches 100;

Length 1684; Indels

19;

Gaps

183

582 123

637

752

694

Query Match Best Local Similarity

7.2%;

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; MOLECULE TYPE:
US-08-762-500-25
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                                                                                                              NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                  TELEPHONE: (508) 872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08 FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                          NAME: Dugan, Deboral REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                      amino acid
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                                                                      1684 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                      Deborah A.
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imothy C.
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US-08-762-500-75; Sequence 75, Ap; Patent No. 6030
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TOPOLOGY: 1; MOLECULE TYPE: US-08-762-500-75
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Best Local Similarity
                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                              SEQUENCE CHARACTERISTICS:
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ADDRESSEE: GENZYME CORPORATION
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                                              TYPE:
                                                                                                                                                                     NAME: Dugan, Deborah A. REGISTRATION NUMBER: 37,315
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/
FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                          LENGTH:
                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
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                                                                                                              (508)
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                                                                                                                          (508) 872-8400
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                                                                                                         872-5415
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Pred. No. 7.3e-16;
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RESULT 12
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO INTILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08
Sequence 3369, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3832
LENGTH: 242
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 LIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNR 243
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                                                                                                                                                                      RQLANESMIMVIVIHE-MNFAKEISDKVVFMADGVVVESGIPQNI----
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Pred. No. 2.3e-16;
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           CLASSIFICATION:
                           FILING DATE:
                                                                                                                                                                   COUNTRY:
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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3369
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PRIOR FILING DATE: 1997-11-08
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nes 77; Conserv
327 VNNQNK 332
                                                  354 VPFKTK 359
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; Pred. No. 1e-15;
66; Mismatches 121
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Sequence 2, Application US/08395246C Patent No. 5773214 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS CORRESPONDENCE ADDRESS: TITLE OF INVENTION: APPLICANT: Peery, Robert B.
APPLICANT: Skatrud, Paul L. ATTORNEY/AGENT INFORMATION NUMBER OF SEQUENCES: APPLICATION NUMBER: CITY: Indianapolis E: Eli Lilly and Company Lilly Corporate Center Peery, Robert B. MULTIPLE DRUG RESISTANCE GENE ASPERGILLUS US/08/395,246C FLAVUS Version #1.25

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US-09-134-001C-3641
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                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                 Sequence 3641, Application US/09134001C Patent No. 6380370
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               CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                              APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: UUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                         FILE REFERENCE: GTC-007
RIOR APPLICATION NUMBER: US 60/055,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 HSNPFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPM 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 LLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 EQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQ--KKVEAV--MAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                        AGV--LVGSGFLR 550
                                                                                                                                                                                                                                                                                                                                                                                                                            DQQENTTGALTATLSAGTKELTG--ISGVTLGTILIVSVNLVASLGVALVIGWKLALVCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDQESQDGLYQKWQMMLAYALHVLPFSVVATMI-FSS--VCY-----WTLGLHPEVARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPFKTKDSPG-----VF-----SKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---RRGIYCDMVEAH-EIKKRYSRYSKRYSQL------LTNLSP----KHNPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALDKASKGRTTIVIAH--RLSTIQKAYNIIVLANGQIVEQGPHEHLMD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMALPNGYDTNIESFSLSG----GQKQRIAIARAIIKDPKILLLDEATSALD-TKSEKLVQ 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·LSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q-----MSLVSQEPRLFAT-TIAENIRY-GIIGSRFEKESTYEIRKRVEAAARMANAHDF 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAHDLSCYIPAGKTTAFVGPSGSGKSTIISLLERFYDPVAGTIMLDGHDIQTLNLRWLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GYFSAALLA--PHLIGEFLTLVLLG--IVQNPNIVNSV------VALLSI 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FKFLASFNRPEWPFLLLGLCASILAGGIQPSQAVLFAKAVSTLSLPPLE----YPKLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----HDANFWCLMFLMIGIVSLVLYSVQGTLFAYSSEKMVYRARSQAFRVILHQDISFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAV 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317-277-1917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.9%; Score 229; DB 1; 1
23.0%; Pred. No. 6.4e-15;
1tive 110; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35784
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                                                                                                                                                                                                                                                                                                                                                                                                                            888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3641
LENGTH: 273
TELEFAX: (508) 872-54 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 27
TYPE: PRT
                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                 TELEPHONE: (508) 872-8400
                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 17-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 ERLNISHLI-----NKNIAELSGGQQQRVLIARALISDPSVLVLDEPTNGIDAKHVSKFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 -IYGHPIQFVD 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 QDCFSYVLQ------SDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27, Application US/08665259
o. 6028173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 SLKISYVSQKASAFNAGFPASYKEVVLSGLTKTKKL-----FQRFNKNDYQ-KVTKVL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 KHYLENINIKINQGEFLAIVGPNGAGKSTLLKVI---LGLLPIQKGEIIYDGKPFKGNKS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 RQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRALRREQF 125
                                                                                                                                                                                                                                                                                                                            01701
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                                                                                                                                                                                                                                                                                                                                                                                                   One Mountain Road
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Van Raay, Terence ...
Klinger, Katherine W.
Klinger, Katherine W.
NOUEL HUMAN CHROMOSOME 16 GENES,
NOUEL HUMAN CHROMOSOME 16 GENES,
NOUEL HUMAN CHROMOSOME 16 GENES,
                                                                                                                                                                                                                                                                                                                                            United States of America
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                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dackowski, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Connors, Timothy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Landes,
                                                                                                                                                                                                                                                                                                                                                                                                                       GENZYME CORPORATION
                                                                                                                                                                                                                                                                                    Floppy disk
               872-5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gregory M.
                                                                                                                                                                                         US/08/665, 259
                                                                                       37, 315
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                                                                         IG5-9.1
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TYPE: amino acid

TRANDEDNESS: not relevant

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-665-259-27
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255 ELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGY 289
| | | :||: | | |: : | | ||
| 1271 ECEALCTRLAIMVNGRLHCLGSIQHLKNRFGD-GY 1304
                                                                                     195 TGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRS 254
| :|::| | |: | : ||||||:|
1212 GGNKRKLSTAIALIGVPAPIFLDEPTTGMDPKARRFLWNLILDLIKTGRSVVLTSHS-ME 1270
                                                                                                                                                                                1161 VPVDELTAREHLQLYTKLRCI----PWKDEAQVVKWALEKLELTKYADKPAGTY-----S 1211
                                                                                                                                                                                                                                                                     137 TLLSSLTVRETLH-YTALLAIRRGNPGSFOKK-VEAVMAELSLSHVADRLIGNYSLGGIS 194
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Search completed: June 11, 2003, 09:14:17 Job time: 22 secs

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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628
622
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615
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614.5
                                                                                                                                                           680.5
672.5
662
                                                                                                                                                                                                                        Score
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                                                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      June 11, 2003, 09:08:12; Search time 39 Seconds
(without alignments)
3439.402 Million cell updates/sec
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3326
         Maximum Match 100%
Listing first 45 summaries
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sp_mammal:*
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sp_unclassified:*
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sp_bacteriap:*
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     Q87543
Q961D6
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O9TO04 mus musculu
O9m3d6 arabidopsis
O8rw19 arabidopsis
O9aru4 oryza sativ
O91182 arabidopsis
O9fnb5 arabidopsis
O9fnb5 arabidopsis
O9fnb6 arabidopsis
O9123 arabidopsis
O9m2v7 arabidopsis
O9zu35 arabidopsis
O9zu35 arabidopsis
O9zu35 arabidopsis
                                                                                                                                                      Q8r543 mus musculu
Q96ta8 homo sapien
Q96ld6 homo sapien
Q8t691 dictyosteli
                                                                                                                                                                                                                     Description
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Q8R543 ID Q8 AC Q8 DT 01 DT 01 DT 01 DE St

RESULT 1

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565	567	571.5	571.5	572	573.5	575.5		578	580.5	581.5	583.5	584·	587.5	587.5	588.5	589.5	591.5	592	595.5	595.5	595.5	597	600	600.5	602.5	809	610
17.0	17:0	17.2	17.2	17.2	17.2	17.3	17.3	17.4	17.5		17.5	17.6	17.7	17.7	17.7	17.7	17.8	17.8	17.9	17.9	17.9	17.9	18.0		18.1	18.3	18.3
1528	626	662	609	739	669	666	649	705	669	687	687	755	646	627	648	646	740	610	785	687	658	590	602	670	654	708	679
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Q8T677	OST684	094914	Q9C8W6	Q9LFG8	Q8WRR1	Q9EPG9	Q9SIT6	Q9LIW1	Q8WRF2	Q9NH94	Q9C8K2	Q9ZUT0	Q8VBS9	Q91WA9	Q9C6W5	Q9C6R7	080946	P90746	Q96L76	Q94960	016574	Q9MAH4	Q9VC15	077423	Q9LIW2	Q9M2V5	09вн97
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ALIGNMENTS

Query Match 21.2%; Score 704; DB 11; Length 673; Best Local Similarity 28.7%; Pred. No. 5.8e-43; Matches 195; Conservative 130; Mismatches 261; Indels 94; Gaps 17;	EMBL; AF351810; AAL82898.1; SEQUENCE 673 AA; 76008 M	DR EMBL; AF351807; AAL62898.1; JOINED. DR EMBL; AF351809; AAL62898.1; JOINED.	EMBL; AF351804; AAL82898.1; EMBL; AF351805; AAL82898.1;	DR EMBL; AF351802; AAL62898.1; JUINED. DR EMBL; AF351802; AAL62898.1; TOTNED. DR EMBL; AF351803: AB162898 1: TOTNED.	EMBL; AF351800; AAL82898.1;	- 	"Molecular cloning, genomic st	RC STRAIN=129/SV;	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxID=10090;	Eukaryota; Metazoa; Chordata;	OS Mus musculus (Mouse).	Sterolin 2.	01-JUN-2002 (TrEMBLrel.	01-JUN-2002 (Tramburel, 21,	<u>.</u>	Ž

11 GSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVR---

-PWWD-I 57

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01-DEC-2001
01-JUN-2002
       "Identification of breast cancer resistant protein/mitoxantrone resistance/placenta-specific, ATP-binding cassette transporter of NB-506 and 7-107088, topoisomerase I inhibitors indolocarbazole structure.";
Cancer Res. 61:2827-2832(2001).
EMBL; AB051855; BAB46933.1;
                                                                                         SEQUENCE FROM N.A. MEDLINE-21201983;
                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                         Q96TA8;
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                                                                        Arakawa H., Nishimura S.
                                                                                 Komatani H., Kotani H.,
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GTVLQDASQGLQDSL---
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
cassette superfamily G (White) member 2
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ni H., Hara Y., N
ABC_transportr.
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                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 3
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D7 01-J
D7 01-J
D7 01-J
D7 01-J
D7 01-J
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01-DEC-2001 (TremBLrel.
01-JUN-2002 (TremBLrel.
ABC transporter ABCG2.
                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
                                                                                                                                                                               Q96LD6
SEQUENCE FROM N.A.
                                                                       Homo sapiens (Human)
                                                                                                                                                               Q96LD6;
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ProDom; PD000006; ABC_transportr;
SMART; SM00203; TK; 1.
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                                          Chordata;
Primates;
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Last annotation update)
                                                                                                                                               Created)
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Pred. No. 2.9e-41;
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                                          Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                               PRT;
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                                          Hominidae;
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                                                      Euteleostomi;
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369 356 312

256

196 129 137 72

18;

189

Length 801; Indels

110;

Gaps

16

120

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RESULT 4
Q8T691
ID Q8T691
AC Q8T6
AC Q8T6
AC Q1-J
DT 01-J
DT 01-J
DT 01-J
DE ABC
GN ABCG
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Best Local Similarity
Dictyostelium discoideum (Slime mold) Eukaryota; Mycetozoa; Dictyosteliida; NCBI_TaxID=44689;
                                                                              ABC transporter AbcG1.
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InterPro; IPR003880; Ppantne_attach.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SEQUENCE 655 AA; 72288 MW; B3B5DC02C095C4A8
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                                 Breast cancer resistance ABCG2 OR BCRP1.
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"Evolution of the ABC transporters of Dictyostelium.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF482380; AAL91485.1;
               Mus musculus
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Q1-MAY-2000 (TrEMBLrel. 21, Last and procession of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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Chordata; Craniata; Vertebrata;
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Pfam; PP00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN 1.
SEQUENCE 657 AA; 73021 MW; 207B70BC272CC0D5
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Cancer Res. 59:4237-4241(1999).
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Allen J.D., Brinkhuis R.F., Wijnholds J., Schinkel A.H.;
"The mouse Bcrpl/Mxr/Abcp gene: amplification and overexpression
cell lines selected for resistance to topotecan, mitoxantrone, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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NCBI_TaxID=10090;
[1]
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                                                                                                   VAYTASSMALAIATGQSVVSVATLLMTIAFVFMMLFSGLLVNLRTIGPWLSWLQYFSIPR
                                                                                                                     IGEFLTLVLLGIVQNPNIVNSVVALLSIAGV--LVGSGFLRNIQEMPIPFKIISYFTFQK
                                                                                                                                                                                                                                                                                   DTQS-----KEREIETSKR-------VQMIESAYKKSAICHKTLKNIERMKHLKTLP
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                                                                                YCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPG 615
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                                                             YGFTALQYNEFLGQEFCPG---FNVTDNSTCVNSYAI----
                                                                                                                                            YISGYYRVSSYFFGKVMSDLLPMRFLPSVIFTCILYFMLGLKKTVDAFFIMMFTLI---M
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               PRELIMINARY;
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           271
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725 AA;
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Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk Hayashizaki Y., Ishida J., Jones T., Kanlya A., Karlin-Neumann G. Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Mirand Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Ecker J.R., Theologis A., Tracy S.E., Shinozaki K., Davis R.W., "Full Lenoth one" - 6
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InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
SMART; SM00382; AAA; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat
ABC transporter-like protein (Putative ABC transporter-1)
T26112.10 OR AT3G55130.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monfort A., Casacuberta E., Puigdomenech P., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                        33 PEPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSSGSGK
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LIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETS----
                                                                                            PKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGE
                                                                                                                                                                               ALLAIRRG-NPGSFQKKYEAVMAELSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQD
                                                                                                                                                  SEFRLPRSLSKSKKMERVEALIDQLGLRNAANTVIGDEGHRGVSGGERRRVSIGIDIIHD
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(FEB-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80656 MW;
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Pred. No. 6e-39;
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Toriumi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lemcke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee
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Matches 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 77.2 kDa protein.
AT3GZ1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. SEQUENCE 691 AA; 77219 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8RWI9;
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                   171
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        GERKRYSIALEILTRPQILFLDEPTSGLDSASAFFVIQALRNIARDGRTVISSVHQPSS
                                        TGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRS
                                                                                        STLTVRETITYSAHLRL----PSDMSKEEVSDIVEGTIIELGLQDCSDRVIGNWHARGVS
                                                                                                             RIMAINGPSGSGKSTLLDSLAGRLARNVVMTGNLLLINGKKARLD--YGLVAYVTQEDVLL
                                                                                                                                                                                               LEGAPATAPE-PHSLGILHASYSVSHRVRPWWDITSCRQQW----TRQILKDVSLYVESG
                                                                                                                                                                                                                                                         LEGSSSGRRQLPSKLEMSRGAYLA-----WEDLTVVIPNFSDGPTRRLLQRLNGYAEPG
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                                                                                                                                                                                                                                                                                                                                             Conservative 123; Mismatches 225;
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                                                                                                                                                                                                                                                                                                                                                                   Score 628; DB 10;
Pred. No. 2.1e-37;
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                                                                                                                                                                                                                                                                                                                                                                                      691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A., Kawai
                                                                                                                                                                                                                                                                                                                                           94;
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                                                                                                                                                                       Query Match
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Matches 171
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01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                     Pfam; PF00005; ABC_tran; 1.
ProDom; PD00006; ABC_transportr; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport.
SEQUENCE 668 AA; 73368 MW; D1875B
                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. EMBL; AP003046; BAB40032.1; -- Interpro; IPR003593; AAA_ATPase. Interpro; IPR003593; AAA_ATPASE. Interpro; IPR003499; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki T., Matsumoto T., Yamamoto K., "Oryza sativa nipponbare(GA3) genomic clone:P0445D12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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118 HLSGFLYINGRPISEGGYK--IAYVRQEDLFFSQLTVRETLSLAAELQLRRTLTPERKES
                                                                                                                                                                       171;
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                                                                                                                                                                                         Similarity
                                                                             -FLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRG-NPGSFQK
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TLKGSQRIQETPATSDPLMNLATSVIKARLVEN-YKRSKYAKSAKSRIRELSNIEGLEME
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1 (TrEMBLrel. 17, I
2 (TrEMBLrel. 21, I
                                                                                                                                                                                                                                                   ; Transport.
568 AA; 733
                                                                                                                                                                       Conservative
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                                                                                                                                                                 18.7%; Score 622; DB 10; 31.0%; Pred. No. 5.4e-37; tive 100; Mismatches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                577
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                          PROSITE; PS00211;
PROSITE; PS00012;
                                                ProDom; PD000006; AB(
SMART; SM00382; AAA;
                                                                               DNA Res. 7:217-221(2000).
EMBL; APPO01313; BAB03081.1; ..
InterPro; IPR003593; AAA_AIPase.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003880; Ppantne_attach.
                                                                                                                                          "Structural analysis of Arabidopsis Sequence features of the regions of TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                 ABC transporter-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                        Pfam; PF00005; ABC_tran;
                                                                                                                                                                                                                                                                                                                                                                                                                      Q9L182;
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                                                                                                                                                                                            MEDLINE-20363099; PubMed-10907853;
                                                                                                                                                                                                                                                         STRAIN-COLUMBIA;
Kaneko T., Kato T.,
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                     Vakamura
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                         PS00012;
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  ΑĄ,
                                                           ABC_transportr; 1.
                        PHOSPHOPANTETHEINE;
                                    ABC_TRANSPORTER;
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Q01-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
ABC transporter-like protein.
Arabidopsis thaliana (Mouse-ar cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            EMBL; AB006704; BAB08684.1; ...
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
                                                             "Structural analysis of Arabidopsis thaliana chromosome 5. Sequence features of the regions of 1,044,062 bp covered by physically assigned Pl clones."; DNA Res. 4:291-300(1997).
                                                                                                                                               STRAIN-COLUMBIA; MEDLINE-98069011; PubMed-9405937;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           Q9FNB5
                                                                                                                         Tabata S.
                                                                                                                                  Kotani H., Nakamura Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --EVSRTFP-----QDQTNARLRKKAITNRWPTSWWMQFSVLLK----RGLKERSHESFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPADFVLDLANGITSDTKQYDQIETNGRLDRLEEQNSVKQSLISSYKKN--LYPPLKE--
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                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
ABC_transportr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.6%;
                                                                                                                                                                                                                                                                                                                                                                                                               -GVQYTWDEVYECGS
                                                                                                                                   Sato
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                                                                                                                                  s.,
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                                                                                                                                   Kaneko
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                                                                                           covered by thirteen
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                                                                                                                                                                                                                                eudicots;
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E
                                                                                                                                                                                                                                             Tracheophyta;
                                                                                                                                   Miyajima
                                                                                                           II.
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                                                                                                                                                                                                                                Rosidae;
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P91892
ID P9189
AC P9189
AC P9189
D7 01-MA
D7 01-MA
D7 01-MA
D7 01-MI
D8 EYE P
GN WHITE
GO ENKAI
OC Ptery
OC Aedes
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OC NCBL
RN [1]
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RN [2]
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RD SEQUE
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Best Local
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                                                                                                                                              P91892;
01-MAY-1997
01-MAY-1997
01-JUN-2002
EYE pigment
                                                                                                    WHITE.

Aedes aegypti (Yellowfever Aedes) Arthroj
Eukaryota; Metazoa; Arthroj
     SEQUENCE FROM N.A.
STRAIN-ROCKEEELLER;
MEDLINE-97418473; PubMed-9272447;
Coates C.J., Schaub T.L., Besansk
                                                                                               Pterygota;
                                                                                                                                                                                                                 P91892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
ATP-binding.
SEQUENCE 727 AA; 80300 MW; 6345CCF5877213
                                                                       NCBI_TaxID-7159
                                                                                                                                                                                                                                                                                                          589
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: :||:||||:||:||: |: |: || |: : : :||:| | |
LAVLGASGSGKSTLIDALANRIAR-GSLKGNVTLNGEVLNSKMQKAISAYVMQDDLLFPM
                                                                                                                                                                                                                                                                                                       SSNVSVTTNPMCAFTQGIQFIEKT
                                                                                                                                                                                                                                                                                                                                GYTIVVAIL--AYFLLESGFFINRDRIPGYWIWFHYISLVKYPYEAVLLNEF----
                                                                                                                                                                                                                                                                                                                                                       --NSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                  PKG-VQERLG-CFAFAMSTTFYTCADALPVFLQERFIFMRETAYNAYRRSSYVLSHSLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKGAIQDRYGLLYQFYGATPYTGMLNAVNLFPYLRAVSDQESQDGLYQKWQMMLAYALHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-----KEREIETSKRVQM-IESAYKKSAICHKTLKNIERMKH-----LKTLPMV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDL-----TSVDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERRRVSIGIDIIHDPILLFLDEPTSGLDSTSALSVIKVLKRIAQSGSMVIMTLHQPSYRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHSLGILHASYSVSHRVRPWW-------DITSCRQQWTRQILKDVSLYVESGQI
                                                                                                                                                                                                                                                                                                                                                                                   LPSLIILSLAFAAITFWGVGLDGGLMGFLFYFLVILASFWAGSSFVTFLSGVV--PHVML
                                                                                                                                                                                                                                                                                                                                                                                                        LPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFL--LFFVLRVRSNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLVEENKGFRQRKAEPRSQTGLSLKEAISASISKGKLVSGATTTTHSSGSSPVSTIPTFA
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                                                                                                                                              7 (TrEMBLrel. 03, 07 (TrEMBLrel. 03, 12 (TrEMBLrel. 21, 12 TANSPORTER (EYE)
                                                                                PRELIMINARY;
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28.7%;
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     Besansky N.J.,
                                                                                                                                             Last sequence update)
Last annotation update)
pigment transporter).
                                                                                                                                                                                      Created)
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Pred. No. 1.
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     Collins
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     F.H.,
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                                                                                                        Insecta
     James
                                                                                              Culicoidea;
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Best Local S
Matches 169
Q8RXNO;
Q8RXNO;
01-JUN-2002
01-JUN-2002
01-JUN-2002
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ProDom; PD00006; ABC_transportr; 1.

TIGREPAMS; TIGR00955; 3a01204; 1.

PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.

SEQUENCE 692 AA; 77231 MW; DF2F00EEB4C176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-1998) to the EMBL/GenBa
EMBL; 088851; AAC04894.1; -
EMBL; AF051096; AAC05165.1; -
InterPro; IPR003439; ABC_transportr.
InterPro; IPR005284; Pigment_Permease.
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[2]
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                                                                               12
                                                                                                                     661
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DFGFDIACLCMLIVIFRL
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                                                                                                                                                                                                                                                                                                                                             SNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYA
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                                                                                                                                                                      EALLINQWSTVQEGDIACTRANV
                                                                                                                                                                                            EILVVNEFYGL---NFTCGSSNVSVTTNPMCAFTQGIQFIEKTCP--GATSRFTMNFLIL
                                                                                                                                                                                                                        VATSFGYLISCASSSISMALSVGPPVIIPFLIFGGFFLNSASVPSYFEYLSYFSWFRYAN
                                                                                                                                                                                                                                                  IVNSVVALLSIAG-----
                                                                                                                                                                                                                                                                        IAEVPLFLAVPFVFTSITYPMIGLKSGAT---YYLTALLIVVLVA-----N
                                                                                                                                                                                                                                                                                                                            QD----GVMNINGALELELTNMTFQNVFAVINVFSAELPVFLREKRSRLFRVDTYFLGKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGKTIILTIHQPSSELYCLFDKILLVAEGRVAFLGSPYQASEFFSQLGIPCPPNYNPADF
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                                                                                                                                           -YSFIPALVILGIVVFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                               YVQMLAI---APNKEAECRDTIKKICDSFAVSPMAREVMEVANSGKNVEEQYYLQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTIIGAPGRMKGLSGGERKRLAFASETLTDPHLLLCDEPTSGLDSFMAHSVLQVLKGMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQ-KKVEAVMAELSLSHVA
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schaub T.L.,
                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.5%; Score 615; DB 5; 27.3%; Pred. No. 1.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L., James A.A.;
to the EMBL/GenBank/DDBJ
  21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135; Mismatches
Last sequence update)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana (Mouse-ear c
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Submitted (OCT-1999)
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00211; ABC_TRANSPORTER; 1. ATP-binding; Transport. SEQUENCE 594 AA; 65939 MW; 5BD2F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr;
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003399; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAC and BAC clones.";
DNA Res. 7:217-221(2000)
517 TLVLLGIVQNPNIVNSVVALLSIAG-VLVGSGFLRNIQEMP-----IPFKIISYFTFQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLKGSQRIQETPATSDPLMNLATSVIKARLVEN-YKRSKYAKSAKSRIRELSNIEGLEME
                                                                                                                                                               LYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFL
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                                                                                                     YYGVSVYILSNYISSFPFLVAISVITGTITYNLVKFRPGFSHYAFFCLNIFFSVSVIESL
                                                                                                                                                                                                                                ----SVGTIFYDVGYS-YTSILARVSCGGFITGFMTFMSIGGFPSFLEEMKVFYKERLSG
                                                                                                                                                                                                                                                                                                AIQDRVGLLYQFVGATPYTGMLNAVNL--
                                                                                                                                                                                                                                                                                                                                                                    IRKGSEATW-WKQLRTLTARSFINMCRDVGYYWTRIISYIVVSI---
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the regions of
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Pred. No. 1.8e-36;
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Best Local
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Bargues M., Collado M.C., Navarro P.,
Mewes H.W., Rudd S., Lemcke K., Mayer
Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding.
720 AA;
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Submitted (APR-2000) to the
EMBL; AL132970; CAB82704.1;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000
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          SVINHGGGTLAVPAFANP---
                                                                                       GGTRGLYEFNKKWQEMKKQSNPQTLTPPASPNP--NLTLKEAISASISRGKLVSGGGGGS
                                                                                                                                                                       SHRVLSLLDRLIFLSRGHTVFSGSPASLPSFFAGFGNPIPENENQTEFALDLIRELEGSA
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IPR003439; ABC_transportr.
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                                             -TLPMVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLL 401
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      -FWIEIKTLTRRSILNSRRQPELLGMRLATVIVTG-FIL
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"Sequence and analysis of chromosome 2 of the plant Arabiaa---'
thaliana.";
                                                                                                                                                                                                                                                PROSITE; PS00211; ABC_TRANSPORTER; 1. ATP-binding; Transport. SEQUENCE 725 AA; 78899 MW; 7DB2E5
                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases | -- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. EMBL, AC006200; AAD14532.1; -- InterPro; IPR003593; AAA_ATPase. InterPro; IPR003439; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                            Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr;
SMART; SM00382; AAA; 1.
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01-MAY-1999
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LSLSPRLHLSGLLEVNGKPSSSKAYK--LAFVRQEDLFFSQLTVRETLSFAAELQLPEIS
                                                                               LGRAGT - - FLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRR - G
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591 IRWAFQGLCINEFSGLKF 608	591	망
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532 VESFAASAMGLTVGAMVPSTEAAMAVGPSLMTVFIVFG-GYYVNADNTPIIFRWIPRASL 590	532	Ф
508 APHLIGEFLTLYLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISTFTF 567	508	Ϋ́
IVDRERSKGSYSLGPYLLSKTIAEIPIGAAFPLMFGAVLYPMARLNPTLSREGKFCGIVT 531	472	В
VSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALL 507	448	Ş
422 SAVIFGSVFWRMGKSQTSIQDRMGLLQVAAINTAMAALTKTVGVFPKERA 471	422	В
388 TRLLQNLIMGLELLEFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRA 447	388	Qy
362 YATPLSMKEETKNGMRPRRKAIVERTDGWWRQFFLLLKRAWMQASRDGPTNKVRARMSVA 421	362	B
'TR	336	Qy
302 REPLTYFGNFGFLCPEHVNPAEFLADLISVDYSSSETVYSSQKRVHALVDAFSQRSSSVL 361	302	B
-EMILDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAIC 335	279	Ϋ́
TTGLDAPQAEKVMETLQKLAQDGHTVICSIHQPRGSVYAKFDDIVLLTEGTLVYAG-PAG 301	243	В
TTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPA- 278	220	δ
SAEERDEYVNNLLLKLGLVSCADSCVGDAKVRGISGGEKKRLSLACELIASPSVIFADEP 242	183	В
160 NPGSFQKKVEAVMAELSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEP 219	160	Qy

Search completed: June 11, 2003, 09:13:23 Job time: 43 secs

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Perfect score:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 182; Conservative 124; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 29.4%;
        415
                                                                                                                                                                           303
                                                                                                                                                                                                                                                                243
                                                                                                                                                                                                                                                                                               211 PKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGE
                                                                                                                                                                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                                                                    124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 TTLLDAMSGRLGRAGTFLGEVYVNG-RALRREQFQDCFSYVLQSDTLLSSLTVRETLHYT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 PEPHSLGILHASYSYSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSSGSGK
                                                                                                                                                                                                                                                       PIVLFLDEPTSGLDSTNAFMVVQVLKRIAQSGSIVIMSIHQPSARIVELLDRLIILSRGK
NPSLFETF-ILAKRYMKNWIRMPELVGTRIATVMVTGC-LLATVYWKLDHTPRGA-QERL
                                        SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRV 420
                                                                                  EKWQQNKISLIQSAPQTNKLDQDRSLSLKEAINASVSRGKLVSGSSRSNPTSMETVSSYA
                                                                                                                                                                       SVENGSPASLPGFFSDFGRPIPEKENISEFALDLV-----RELEGSNEGTKALVDFN
                                                                                                                                                                                                                                                                                                                                            SEFRLPRSLSKSKKMERVEALIDQLGLRNAANTVIGDEGHRGVSGGERRRVSIGIDIIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                     STLIDALAGRVAE-GSLRGSVTLNGEKVLQSRLLKVISAYVMQDDLLFPMLTVKETLMFA
                                                                                                                                                                                                               LIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVPYVLNENNLQYDVTLRRR----FGFSRQNGVKTLLDDVSGEASDGDILAVLGASGAGK
                                                                                                                            -----KRVQMIESAYK-------KSAICHKTL--KNIERMKHLKTLPMVPFKTKD 360
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Result No.

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410	413	417.5	418.5	420	421	425	425.5	429	435	454.5	456.5	464	488	497	504
12.3	12.4	12.6	12.6	12.6	12.7	12.8	12.8	12.9	13.1	13.7	13.7	14.0	14.7	14.9	15.2
1177	1413	1619	1420	1435	1450	1451	1443	1469	668	675	1426	1450	737	547	695
_	N	N	N	N	Ν	N	N	N	N	بــر	N	ν	N	2	2
D71416	G84790	T30541	T02644	D96693	T45888	B86286	T02491	н96622	S55023	FYFFB	T30567	A84780	T46101	T31543	T21109
probable PDR5-like	ABC tr	ABC1 transport pro	ABC-type transport	protein Putative A	ABC transporter-li	F9L1.15 protein -	probable ABC trans	probable ABC trans	brown protein - fr	brown protein - fr	ATP-binding casset	probable ABC trans	ABC transporter-li	hypothetical prote	hypothetical prote

ALIGNMENTS

A;Map position: 3 A;Note: T26112.10 C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; A; Molecule type: DNA
A; Residues: 1-725 <MON>
A; Cross references: EMBL: AL132954 ABC transporter-like protein - Arabidopsis thallana N;Alternate names: protein T26112.10 C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000 C;Accession: T47652 R;Monfort, A; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Msubmitted to the Protein_Sequence Database, February 2000 Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer he Protein_Sequence Database, February 2000 cultivar Columbia; Score 649.5; Pred. No. 1e BAC clone T26I12 DB 2; Length 725;

1e-40;

246; Indels 67;

Gaps

270

242 210

319 302 182

123

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A; Residues: 200-1294 <ALF>
A; Cross-references: EMBL:Z74817
A; Experimental source: strain S288C
A; Note: this sequence has been revised in reference S77690
A; Note: this was assumed to be the complete sequence of pro C; Genetics:
A; Cross-references: SGD:S0005435
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                                                                                                                                                                                                                                                F;710-916/Domain: ATP-binding cassette homology <ABC2>
F;727-734/Region: nucleotide binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position:
A; Note: YOL075c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein YOL075c - yeast (Saccharomyces cerevisiae)
W;Alternate names: hypothetical protein 01125; hypothetical protein 01130; }
C;Species: Saccharomyces cerevisiae
C;Date: 21-Apr-1997 #sequence_revisiae
C;Accession: S77690; S66767; S66768
R;Alexandraki, D.; Katsoulou, C.; Tzermia, M.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                    F;469-485/Domain: transmembrane #status predicted <TM2>F;496-512/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                       F;62-69/Region: nucleotide-binding motif A (P-loop) F;376-392/Domain: transmembrane #status predicted <
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                                                                                                                                                                                                            F;1125-1141/Domain: transmembrane
                                                                                                                                                                                                                                                                                              F; 496-512/Domain:
F; 606-622/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Note: this is a revision A:Accession: S66767 A:Molecule type: DNA
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                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology Keywords: ATP; nucleotide binding; P-loop; transmembrane protein 45-263/Domain: ATP-binding cassette homology <ABC1>
                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: DNA
Residues: 1-179, 'TTRTGVFLVVKRED'
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Residues: 1-1294 <ALE>
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Residues: 200-1294 <ALF>
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                                                                                                                                                                                          -1193/Domain:
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                                               5
                                                                                         181;
                                                                                                            Similarity
TKEILQSVNAIFKPGMINAIMGPSGSGKSSLLNLISGRL-KSSVFAKFDTSGSIMFNDIQ
                       TRQILKDVSLYVESGQIMCIIGSSGSGKTTLLDAMSGRLGRAGTFL-----GEVYVNGRA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCFVRGVQVFDSTLLGGVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATM
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                                                                                      Conservative
                                                                                                                                                                                                                                                                                          transmembrane #status predicted <TM3>
transmembrane #status predicted <TM4>
                                                                                                                                                                  transmembrane #status predicted <TM5>
transmembrane #status predicted <TM6>
transmembrane #status predicted <TM79-
transmembrane #status predicted <TM79>
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                                                                                                   18.9%; Score 627; DB 2; 31.7%; Pred. No. 1.1e-38;
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                                                                                      106;
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                                                                                    Mismatches
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YOL074c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of protein YOL075c
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                                                                                                                         Length 1294;
                                                                                  Indels
                                                                                  56;
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                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 LRREQFQDCFSYYLQSDT-LLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLS
FAFPGNLKLTCEDGGKNSDGT----CEFANG 1250
                                                        NEFYG-LNFTC--GSSNVSVTTNPMCAFTQG
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                                                                                                          MINTFFERPGFVVNCISIILSIGTOMSGLMSL----GMSRVLKGFNYLNPVGYTSMIIIN
                                                                                                                                                               VILGIVQNPN-IVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVV
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                                                                                                                                                                                                                                                                                                                                                                                                  FFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKW 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQYSQESFFTEYSEFVRK-PANLVLAYIVNVKRQFTTTRRSFDSLMARIAQIPGLGVIFA
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A;Molecule type: DNA
A;Residues: 1-1049 <GOF>
A;Residues: 1-1049 <GOF>
A;Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42328.1; PI
R;Purnelle, B.; Skala, J.; Goffeau, A.
Yeast 7, 867-872, 1991
Yeast 7, 867-872, 1991
A;Title: The product of the YCR105 gene located on the chromosome A;Reference number: S40914; MUID:92160395; PMID:1789009
A;Accession: S40914 ATP-dependent permease ADP1 precursor - yeast (Saccharomyces N;Alternate names: protein YCR011c; protein YCR105 C:Species: Saccharomyces cerevisiae C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_chan C;Accession: S19421; S40914 R;Goffeau, A.; Purnelle, B.; Skala, J. submitted to the Protein Sequence Database, A; Accession: S19421 A; Reference number: S19420 31-Mar-1992 #text_change March 1992 cerevisiae) PID:g1907154; GSPDB 19-Jan-2001

A; Status: not compared with

from Saccharon

A; Residues: 1-1049 < PUR> R; Skala, J.; Purnelle, B Molecule type: DNA J.; Purnelle, 409-417, 1992 B.; Goffeau, conceptual

A; Reference number: S25353; A; Title: genes The complete sequence of a 10.8 kb MUID:92327849; PMID: 1626432 segment distal of SUF2 on

the right arm

A; Contents: annotation

Yeast 8,

A; Gene: SGD: ADP1; MIPS: YCR011c C; Genetics:

A;Cross-references: SGD:S0000604; MIPS:YCR011c

A.Map position: 3R
C.Superfamily: ATP-dependent permease ADPL, ATP-binding cassette homology
C.Superfamily: ATP: qlycoprotein; nucleotide binding; P-loop; transmembrane F;1-25/Domain: signal sequence predicted protein

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F;938-954/Domain: transmembrane #status predicted <TM6>
F;938-954/Domain: transmembrane #status predicted <TM7>
F;1025-1041/Domain: transmembrane #status predicted <TM7>
F;50,114,165,221/Binding site: carbohydrate (Asn) (covalent) #status
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Best Local Similarity
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 1015
                                   625
                                                                  186
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                                                                                                                                                                                                                            MMLAYAL----HVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLT
                                                                                                                                                           LVLLGIV---QNPNIVNSVVALLSIAGVLVGSGFLRNIQEMP-IPFKIISYFTFQKYCSE
                                                                                                                                                                                             --LATYISKIMSEVPPLRVPPPILLSLIVYPMTGLNMKDNAF-PKCIGILLENLGISLE
                 LILYSFIPALVILGI--VVFKIRDHL
                                                                  SLLINEVRTLMLKERKYGLNI-
                                                                                                                                                                                                                                                                 NV-SNDISG-FQNRMGLEFFILTYFGFVTFTGL----SSFALERIIFIKERSNNYYSP--
                                                                                                                                                                                                                                                                                               RVRSNVLKGAIQDRVGLLY---QFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQ
                                                                                                                                                                                                                                                                                                                                  GDLPT-----GQQSAGFLQQLSILNSRSFKNMYRNPKLLLGNYLLTILLSLFLGTLYY
                                                                                                                                                                                                                                                                                                                                                                   KHLKTLPMVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLELLFFVL
-VVQNLVFDIKILALFNVVFLIMGYL
                                                                                                     ILVVNEF ---
                                                                                                                               ILTIGIIFEDLNNSIILSVLVLL---GSLLFSGLFINTKNITNVAFKYLKNFSVFYYAYE
                                                                                                                                                                                                                                                                                                                                                                                                      SLLRDEEDVEGTDGRRGATEIDLNTKLLHDKYKDSVYYAELSQEIEEVLSEGDEESNVLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR-RNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKK---VEAVMAELSLSHVADRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.7%; Score 621; DB 1; Length 1049, 28.6%; Pred. No. 2.3e-38; Live 111; Mismatches 223; Indels 1:
                                                                                              -YGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPGATSRFTMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *status predicted <TM2>
*status predicted <TM3>
*status predicted <TM4>
*status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                        -ETSKRVQMIESAYKKSAICHKTLKNIERM-----
                               648
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                                                                -EVPGATILSTFGF
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T47648
ABC transporter-like protein - Arabidopsis thaliana
N;Alternate names: protein T15C9.80
C;Species: Arabidopsis thaliana (mouse-ear cress)

probable ABC transporter [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: C84423

Rounsley, S.D.; Shea, T.r.

T.P.;

Benito, M.I.;

I.; Town, C.D.; Fujii, S.E.; Umayam, L.; Tall

VanAken,

Koo, H.; Moffat,

RESULT C84423

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R;Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24470
A;Accession: T47648
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A; Note: T15C9.80
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A;Molecule type: DNA
A;Residues: 1-720 < MEM>
A;Cross-references: EMBL:AL132970
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Matches
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                                                                                               GIVQNPNIV----NSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVN
                                EFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKT 612
                                                                GVV--PHVMLGYTIVVAIL--AYFLLFSGFFINRDRIPQYWIWFHYLSLVKYPYEAVLQN
                                                                                                                                  SYVLSHAIVTEPSLIFLSLAFAVTTFWAVGLEGGLMGFLFYCLIILASFWSGSSFVTFLS
                                                                                                                                                               QMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLL
                                                                                                                                                                                                ATVEWRLDNSPKG-VQERLG-FFAFAMSTMFYTCADALPVFLQERYIFMRETAYNAYRRS
                                                                                                                                                                                                                                                                                                                                  GGTRGLVEENKKWQEMKKQSNPQTLTPPASPNP--NLTLKEAISASISRGKLVSGGGGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSLDGDNDHLMRPVPFVLSFNNLTYNVSVRRKLDFHDLVPWRRTSFSK---TKTLLDNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSLEG--APATAPEPHSLGILHASYSVS-----HRVRPWWDITSCRQQWTRQILKDVS
                                                                                                                                                                                                                                 FFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKW
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 SDPTECFVRGVQLFDNS
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White,

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submitted to the Protein Sequence Datab
A; Reference number: 224470
A; Accession: T47650
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-708 <MEN>
A; Cross-reference
                                                                                                                                ABC transporter-like protein - Arabidopsis thaliana 
%;Alternate names: protein T15C9.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
C;Accession: T47650
R;Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-725 <STO>
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Nature 402, 761-768, 199
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Best Local
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Local Similarity 29.7%;
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                                                                                                                                                                                                                                                                                                                        IRWAFQGLCINEFSGLKF 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGRAGT - - FLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRR - G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRPVTIRWRNITCSLSDKSSKSVRFLLKNVSGEAKPGRLLAIMGPSGSGKTTLLNVLAGO
                                                                                                                                                                                                                                                                                                                                                         QKYCSEILVVNEFYGLNF 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVDRERSKGSYSLGPYLLSKTIAEIPIGAAFPLMFGAVLYPMARLNPTLSRFGKFCGIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SA-----VIFGSVFWRMGKSQTSIQDRMGLLQVAAINTAMAALTKTVGVFPKERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YATPLSMKEETKNGMRPRRKAIVERTDGWWRQFFLLLKRAWMQASRDGPTNKVRARMSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEPLTYFGNFGFLCPEHVNPAEFLADLISVDYSSSETVYSSQKRVHALVDAFSQRSSSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGLDAFQAEKVMETLQKLAQDGHTVICSIHQPRGSVYAKFDDIVLLTEGTLVYAG-PAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999
                                                                                                               Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 610.5;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 244;
                                                                                                               April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6e-38;
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R; Pepling, M.; Mount, S.M.

Nucleic Acids Res. 18, 1633, 1990
A; Title: Sequence of a cDNA from th
A; Reference number: S08635; MUID:90
A; Accession: S08635
A; Molecule type: mRNA
A; Residues: 1-687 < PEP>
                                       A;Cross-references: EMBL:X51749; NID:g8825; PIDN:CAA36038.1; R;O'Hare, K.; Murphy, C.; Levis, R.; Rubin, G.M. J. Mol. Biol. 180, 437-455, 1984
                                                                                                                                                                                                                                                                white protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Decies: Drosophila melanogaster
C;Date: 31-Dec-1990 #sequence_revision 17-Feb-1995 #text_change 19-Jan-2001
C;Accession: S08635; S07263; S10240
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A; Title: DNA sequence of the white locus of Drosophila melanogaster A; Reference number: S07263; MUID:85134865; PMID:6084717
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A;Note: T15C9.110
C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DDPSRCFVKGVQVFDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSVTTNPMCAFTQGIQFIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YMVTIAYLSYCLLLGGFYINRDRIPLYWIWFHYISLLKYPYEAVLINEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ~VVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTRDLVEFNEKWQQNQTARATTQSRVSLKEAIAASVSRGKLVSGSSGANPISMETVSSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDL-----TSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGERRRYSIGIDIHDFILLFLDEPTSGLDSTNAFMYVQVLKRIAQSGSVVIMSIHQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STGERRRYSIAAQLLQDPKYMLFDEPTTGLDCMTANQIVYLLYELARRNRIVYLTIHQPR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDLLFPMLTVKETLMFASEFRLPRSLPKSKKMERVETLIDQLGLRNAADTVIGDEGHRGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNG-RALRREQFQDCFSYVLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRGSQSSLEGAPA--TAPEPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QSKEREIETSKRVQMIE----SAYKKSAICHKTLKNIERMKHLKTLP
                                                                                                                                                                            from the Drosophila melanogaster white gene MUID:90221897; PMID:2109311
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36; Mismatches 256:
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591

563 532 472

447

412

397 352 337

277

193

134 157

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A;Cross-references: FlyBase:FBgn0003996
A;Introns: 24/3; 116/1; 334/2; 439/3; 483/3
C;Superfamily: fruit fly white protein; ATP-binding cassette homology
C;Reywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F;113-317/Domain: ATP-binding cassette homology <ABC>
F;130-137/Region: nucleotide-binding motif A (P-loop)
F;261-265/Region: nucleotide-binding motif B
F;67,93,472,554,651/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-24, 'LIFEIPYHCRYTAD',30-687 <OHA2>
A;Cross-derences: EMBL:X02974; NID:g10873; PIDN:CAA26716.1; PID:g10874
A;Experimental source: strain Canton S
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-24, 'LIFEIPYHCRVTAD',30-334,'ITLHLNSYPAWVPSVLPTTIRRTFTYRCWPLCPDGRSSPVIGSPRY
A;Cross-references: EMBL:X02974
A;Experimental source: strain Canton S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S10240
A; Accession: S10240
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Best Local Similarity
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                                                         656 DLPLDYVGLAIL-IVSERVLAYLALR
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                                                                                                                                                                                                    LVVNEFYGL---NFTCGSSNVSVTTNPMCAFTQGIQFIEKTCP--GATSRFTMNFLILYS 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSP------GVESKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLEL-LEFVLRVRSN 410
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                                                                                                                                                                                                                                                                                                           NSVVALLSIAG-------VLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEI 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTK
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                                                                                                                                                                LLINQWADVEPGEISCTSSNT-
                                                                                                                                                                                                                                                         TSPGYLISCASSSTSMALSVGPPVIIPFLLFGGFFLNSGSVPVYLKWLSYLSWFRYANEG
                                                                                                                                                                                                                                                                                                                                                                  ELPLFLTVPLVFTAIAYPMIGLRAGVLHF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                V---GVMNINGAIFLFLTNMTFQNVFATINVFTSELPVFMREARSRLYRCDTYFLGKTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQPENGYTYKATWFMQFRAVLWRSWLSVLKEPLLVKVRLIQTTMVAILIGLIFLGQQLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKGKTVILTIHQPSSELFELFDKILLMAEGRVAFLGTPSEAVDFFSYVGAQCPTNYNPAD
                                                                                                        FIP----ALVILGIVVFKIRDHLISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMQARCAYVQQDDLFIGSLTAREHLIFQAM--VRMPRHLTYRQRVARVDQVIQELSLSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%; Score 602.5; DB 1; 11arity 28.8%; Pred. No. 3.2e-37; Conservative 131; Mismatches 220;
                                                            680
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                                                                                                                                                        TCPSSGKVILETLNFSA--A 655
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A;Residues: 1-590 <STO>
A;Cross-references: GB:AE005173; NID:g7769856; PIDN:AAF69534.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kaiti, R.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Rathors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein F12M16.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
B96573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: fruit fly white protein; ATP-binding cassette homo:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: F12M16.17
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 PATAPEP-----HSLGILHASYSVSHRVRPWWDITS-CRQQWTRQILKDVSLYVESGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PVKAPIPGGREISYRLETKNLSYRIGGNTPKFSNLCGLLSEKEEKVILKDVSCDARSAEI
TSRETMNFLILYSEIPALVILGIVVFKIR 645
                                                                                                                                                                       DGFLYFSLVIWIVLLMSNSEVACESALVPNFIMGTSVISGL-MGSFFLFSGYFIAKDRIP
                                                                                                                                                                                                                                                                              EGLPIFLQDRRILMRETSRRAYRVLSYVLADTLIFIPFLLIISMLFATPVYWLVGLRREL
                                                                                                                                                                                                                                                                                                                          NAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMD----LTSVDTQSKEREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELA-RRNRIVVLTIHQPRSELFQLF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLLSS
                                                                                                                      IPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPGA
                                                                                                                                                                                                                         ARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMP
                                                                                                                                                                                                                                                                                                                                                                               KNIFRTKQLFTTRALQASIAGLILGSIYLNV-GNQKKEAKVLRTG-FFAFILTFLLSSTT
                                                                                                                                                                                                                                                                                                                                                                                                                              RNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKDSPGVFSKLGVLLRRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SCYGHS----KTWKSC----YISAGGELHQSDSHSNSVLEEVQILGQRSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGVELVHDPNVILIDEPTSGLDSASALQVVTLLKDMTIKQGKTIVLTIHQPGFRILEQI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTVQETLTYSALLRLKTKRKDA-AAKVKRLIQELGLEHVADSRIGQGSRSGISGGERRRV
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A;Introns: 115/3; 158/3;
C;Superfamily: fruit fly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-658 <FAV>
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A; Reference number: Z21104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ubmitted to the EMBL Data Library, July 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Caenorhabditis elegans
Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000
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                                                                                                                                                                                                                              LHVLPFSVVATMIFSSVCYWTIGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPN 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCG--YPCPEHSNPFDFYMDLTSVD 308
GLVALKIR 653
                               GIVVFKIR 645
                                                                                                                                                                        IVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCG
                                                                                                                                                                                                        LAELPQYTILPMIYGTIIYWMAGLVASVTSFLVFVFVCITLTWVAVSIAYVGACIFGDEG
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                                                                       CDLI---
                                                                                                 SSNVSVTTNPMCAFTQGIQFIEKTCP-----GATSRFTMNFLILYSFIPALVIL
                                                                                                                                      LVVTFMPMF-VLPMLVFGGFYVNANSIPVYYQYVSFVSWFKHGFEALEANQWKEIDKISG
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27.1%; Pred. No. le
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                                                               -CPASDGPGILTRRGIDTPLYANVLILFMSFFVYRII
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F;110-310/Domain: ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AC004218; NID:g3355463; PIDN:AAC27826.1; PID:g3355464
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallo
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T02567; T00545; C84816
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Retchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A;Reference number: Z14679
A;Accession: T02567
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C;Superfamily: Arabidopsis thaliana probable ATP-binding
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A;Molecule type: DNA
A;Residues: 1-362 <ROW>
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A;Accession: T00545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: cultivar Columbia R; Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: At2g39350; T16B24.1; F12L6.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-740 <STO>
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A; Residues: 1-740 < ROU>
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C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross references: EMBL:AC004697; NID:g3402671; PIDN:AAC28975.1; PID:g3402672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                      SLTVRETLHYTALLAIRRGNPGSFOK-KVEAVMAELSLSHVADRLIGNYSLGGISTGERR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHSLGILHASYSVSHRVRPWWD------ITSCRQQWTRQILKDVSLYVESGQ
GTRGLIEFNKKWQEMKKQSNRQPPLTPPSSPYPNLTLKEAIAASISRGKLVSGGESVAHG
                                                                                                    LDRLIFLSRGHTVYSGSPASLPRFFTEFGSPIPENENRTEFALDLI-----
                                                                                                                                                 FDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKERE----
                                                                                                                                                                                                    RVSIGIDIIHDPILLFLDEPTSGLDSTSAFWVVKYLKRIAQSGSIVIMSIHQPSHRVLGL
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27.5%;
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Pred. No. 2.4e-36;
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		Qy 44 SYSVSHRVRPWWDITSCROOWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRL 103	C;Superfamily: fruit fly white protein; ATP-binding cassette homology C;Keywords: ATP; nucleotide binding; P-loop P;61-253/Domain: ATP-binding cassette homology <abc> F;78-85/Region: nucleotide-binding motif A (P-loop) Query Match 17.8%; Score 590.5; DB 2; Length 638; Best Local Similarity 26.3%; Pred. No. 2.3e-36; Matches 164; Conservative 142; Mismatches 266; Indels 51; Gaps 14;</abc>	submitted to the EMBL Data Library, August 1995 A; Reference number: H00769 A; Accession: G02068 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-638 <cro> A; Cross references: EMBL:U34919; NID:g1314276; PIDN:AAC51098.1; PID:g1314277 C:Genetics: Vhite</cro>	1 molog - human s: Homo sapiens (man) 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 02-Feb-2001 lon: G02068	Db 644 FSDATKCFVRGVQIFDNTPLGELPEVMKLKLLGTVSKYSVTINPMCAFTQG	**************************************	347HKTLPMVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLINGLFLLF
Qy 230 QIVVLLVELARRIRVIVITIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGY 289	در در در در د	Local Similarity 29.9%; pred. No. 2.8e-36; 25 183; Conservative 112; Mismatches 246; Indels 71; Gaps 10 GGSMGLQVNRGSQS-SLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSCR 1	Molecule type: DNA Molecule type: DNA Residues: 1-646 <570> Cross-references: GB:AE Genetics: Map position: 1 Superfamily: Arabidopsi: Query Match	Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Mar Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Scattle: Dreliminary	C86441 probable ABC transporter [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C86441 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewa ansen, N.F.; Hughes, B.; Huizar, L.		Qy 505 ALLAPHLIGEFLILVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISY 564 :: : : : : : : : :	Db 328 WHRPSEEVKQTKRLKGLRKDSSSMEGCHSESASCLTQFCILFKRTELSIMRDSV 381 Qy 385 AVITRLQNLIMGLELLEFVLRVRSNVLKGAIQDRVGLLYQFVGATFYTGMLNAVNLFPV 444

QY 248 THQPESELFCLEDKIAILSFGELIFCGEPEMSLDEFNDGSYPCPEHSNPPDFWDLTSV 307	OY 13 LOSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSHVADRLIGN 187 18	21 79 73 138		of the plant Arabidopsis thalian 0:10617197 PIDN:AAC98055.1; GSPDB:GN00139	RESULT 13 G84791 G84791 G84791 C; Species: Arabidopsis thaliana (cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C; Accession: G84791 R; Lin, X; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M; Koo, H; Moffat, K.S; Cronin, L.A.; Shen, M; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter in the control of the con	OY 575 LVVNEFYGLNFT 586	QY 516 LTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKI-ISYFTFQKYCSEI 574	AYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEF :	QY 396 MGLELLFEVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFEVLRAVSDQESQD 455	OY 340 KNIERWK-HLKTLPMVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLI 395 :	QY 290 PCPEHSNDEDEYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTL 339
			A; Positions: 1,987 (STO) A; Cross-references: GB:AE005173; NID:g10092349; PIDN:AAG12758.1; GSPDB:GN00141 C; Genetics: A; Gene: F5D21.6 A; Map position: 1 C; Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; i	70 00 0C C	; O.;			OF THE TOTAL THE PARTY OF THE P	483 LATMETNL-DNSPKGA-QERLG-FFAFAMSTTFYTCAEAIPVFLQERYIFMRETAYNAYR		Db 371releystegtkplvefhkqwrakqapsynnnnkrntnysslkeaitasisrgk 423 Qy 353wvp-fktkdspgvfsklgvllrrvtrnklavitrllqnlimglf 399

523 LITGAGIIGIIMMTSGFFRLLPDLPKVFWRYPISFMSYGSWAIQGAYKNDFLGLEF 578	533 VVALLSIAG-VLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNF 585		473 PESVVATMIESSVCYWTLGLHPEVAREGYESAALLAPHLIGEELTLYLLGIVONPNTVNS 532	405 SYTSILARVSCGGFITGFMTFMSIGGFPSFIEEMKVFYKERLSGYYGVSVYIISNYVSSF 464	423 LYQFVGATPYTGMLNAVNLFPVLRAVSDORSODKILYOKKOMMIAVALIKVI. 472	358 TWFKQLRTLTKRSFVNMCRDIGYYWSRIVIYIVVSFCVGTIFYDVGH 404	363 GVFSKLGVLLRRVTRNLVRNKLAVITRLLONLIMGLELLFFVLRVRSNVLKGATODRVGL 422	299 RETPATSDPLMNLATSEIKARLVEN-YRRSVYAKSAKSRIRELASIEGHHGMEVRKGSEA 357	323QMIESAYKKSAICHKTLKNIERWKHLKTLPWYPFKTKDSP 362
Search completed: June 11, 2003, 09:13:51 Job time : 25 secs	Db 612 EDAKLYMDELVLGIFFLALRLLAYLVLRYR 641	Oy 616 ATSRETMUFLILYSEIPALVILGIVVEKIR 645	Db 562 LQWSSYLSTVRYGFEGVILT-IYGMERGDLTCLEERCPFREP-QSILRALDV 611	QY 559 FKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPG 615	Db 503 FLLFSALATATALVAQSLGL-LIGAASNSLQVATFVGPVTAIPVLLFSGFFVSFKTIPTY 561	QY 499 FGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIP 558	Db 443 VLTFPLEMAVEMREHLNYWYSLKAYYLAKTMADVPFQVVCPVVYCSIVYMNTGQPAETSR 502	QY 439 VNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVAR 498	Db 385 ILRDTVLTHLREMSHVVIGVLIGLLYLHIGDDASKVENNTGCLEFSMLFLMFAALMPT 442

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379 LVRNKLAVITRLLQNLIMGLELLFEVLRVRSNVLKGAIQDRVGLLYQFYGATPYTGMLNA 438

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Result
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Maximum Match 100%
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Copyright (c) 1993 - 2003 Compugen Ltd.
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236	236.5	238.5	238.5	239.5	239.5	239.5	240	240	240	240	241.5	263	263.5	268	270.5	374	398	403.5	485	562.5	567.5	570.5	578	578.5	585.5
7.1	7.1	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.3	7.9		8.1	8.1	11.2	12.0	12.1	14.6		17.1	_	17.4	17.4	17.6
203	385	1642	1594	2436	2436		1280		1280	1279	247	241	345	242	306	1511	1501	.1564	545	646	646	646	604	627	646
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US-10-252-819-17	US-09-769-787-144	US-09-971-121-2	US-09-971-121-4	US-09-795-693-8	US-10-199-485-8	US-10-156-239-8	US-09-866-866A-4	US-09-866-866A-2	US-10-072-621-7	US-10-097-340-2	US-09-738-626-5108	US-09-815-242-11194	US-09-815-242-11068	US-09-769-787-83	US-09-738-626-4554	US-09-801-368-250	US-09-801-368-346	US-09-801-368-244	US-10-083-357-1335	US-10-154-452-8	US-10-090-455-13	US-10-154-452-4	US-09-745-763-197	US-10-090-455-8	US-10-090-455-2
	144	ν.	4	е 8	8	8, Appli	4	Sequence 2, Appli	7,	'n	5	11194,	e 110	83, Ac	4554,	250,	Sequence 346, App	e 244,	133	B A	13,	1, Appli	Sequence 197, App	8	Sequence 2, Appli

ALIGNMENTS

GENERAL INFORMATION:
APPLICANT: Chen, Hongyun
APPLICANT: Le Bihan, Stephane
TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER
FILE REFERENCE: 100103.406 CURRENT APPLICATION NUMBER: US/10/090,455
CURRENT FILING DATE: 2002-03-01 121 RREQFODCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSHV 6, Application US/10090455 fon No. US20030027259A1 1 MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSC . RQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRAL ADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR RREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSHV RNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDF MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSC for Windows Version 100.0%; Score 3326; 100.0%; Pred. No. 1 0; Mismatches DB 9; .6e-289; AND 0 Indels Length 651; 0; Gaps 180 120 240 180 120 60 0

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APPLICANT: Board of Regents, The University
TITLE OF INVENTION: ABCG5 and ABCG8: Composi
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
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APPLICANT: Shan,
APPLICANT: Barnes
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NUMBER OF SEQ ID NOS: 13
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TYPE: PRT
ORGANISM: Homo sapiens
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Tian, Hui
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Pred. No. 1.6e-289;
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LENGTH: 651
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: Schul
APPLICANT: Shan,
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                                                                                                                                               Query Match
Best Local
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Sitosterolemia Susceptibility TiTLE OF INVENTION: and Methods of Use FILE REFERENCE: 018781-006020US CURRENT APPLICATION NUMBER: US/09/837,992 CURRENT FILING DATE: 2001-04-18 PRIOR APPLICATION NUMBER: US 60/198,465 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/204,234 PRIOR FILING DATE: 2000-05-15
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Pred. No. 1.6e-289;
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Compositions

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Gaps

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APPLICANT: Tularik inc.

APPLICANT: Board of Regents, The University of Texas System
fitte OF INVENTION: ABGC5 and ABGC8: Compositions and Methods of Use
FILE REFERENCE: 018781-007320US

CURRENT APPLICATION NUMBER: US/09/989,981A

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/252,235

PRIOR APPLICATION NUMBER: US 60/252,235

PRIOR APPLICATION NUMBER: US 60/253,645

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEG ID NOS: 13

SOFTWARE: Patentin ver. 2.1

SEG ID NO 2

LENGTH: 652
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                                                               Matches
                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hobbs, Helen H.
APPLICANT: Shan, Bei
APPLICANT: Barnes, Robert
APPLICANT: Tian, Hui
                                                                                                                                                    ORGANISM: Mus musculus FEATURE:
                                                                                                                                     OTHER INFORMATION: mouse ABCG5 (mABCG5)
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                                                                            Similarity
MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEP-HSLGILHASYSVSHRVRPWMDITS
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                                                                          82.5%;
                                                          Score 2744.5; DB 9;
Pred. No. 2.2e-237;
4; Mismatches 64;
                                                                                        Length 652;
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                                                          Gaps
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APPLICANT: Tian, Hui
APPLICANT: Schultz, Joshua
APPLICANT: Shan, Bei
APPLICANT: Shan, Bei
APPLICANT: Shan, Bei
TITLE OF INVENTION: Sitosterolemia Susceptibility Gen
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT APPLICATION NUMBER: US/09/8465
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-15
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-837-992-1
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1.FNGTH: 652
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09837992 Patent No. US20020081687A1
                                                                                                                                                                                                                                                                                                                                                                                                           FULT 5
-09-837-992-1
                                                                                                                       NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2
                                                   LENGTH: 652
TYPE: PRT
ORGANISM: Mus musculus
                                                FEATURE:
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|DPGMFGKLGVLLRRVTRNLMRNKQAVIMRLVQNLIMGLFLLFYLLRVQNNTLKGAVQDR
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            mouse sitosterolemia amino acid sequence
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                           susceptibility
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Query Match

82.5%; Score 2744.5; DB 10; Length 652;

Best Local Similarity 80.2%; Pred. No. 2.2e-237;

Matches 523; Conservative 64; Mismatches 64; Indels 1; Gaps
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APPLICANT: Tian, Hui
APPLICANT: Tian, Hui
APPLICANT: Tolarik Inc.
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION. ABCG5 and ABCG8: Compositions and Methods o
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR APPLICATION NUMBER: US 60/252,356
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-989-981A-4
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09989981A Publication No. US20030049730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hobbs, Helen H. APPLICANT: Shan, Bei APPLICANT: Barnes, Robert
     OTHER INFORMATION: mouse ABCG8 (mABCG8)
                                       ORGANISM: Mus musculus
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Tian, Hui
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-455-7
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                                                                                                                                                                                                                                             Sequence 7, Application US/10090455 Publication No. US20030027259A1 GENERAL INFORMATION:
                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7 LENGTH: 673
                                                                                                         CURRENT APPLICATION NUMBER: US/10/090,455
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                               APPLICANT: Chen, Hongyun
APPLICANT: Le Bihan, Stephane
TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND
FILE REFERENCE: 100103.406
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        NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. (
SEQ ID NO 8
LENGTH: 673
                                                                                                                                                          APPLICANT: Barnes, Robert
APPLICANT: Tilan, Hui
APPLICANT: Trian, Hui
APPLICANT: Tolarik Inc.
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Method
FILE REFERENCE: 018781-0073200S
CURRENT APPLICATION NUMBER: 05/09/989,981A
COURENT FILING DATE: 2002-07-23
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
                                                                                 PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                               APPLICANT: Hobbs, Helen H. APPLICANT: Shan, Bei
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                                                                                                                                                                                                                                                            Sequence 1, Application US/09961086 Publication No. US20030036645A1 GENERAL INFORMATION:
                                                                           APPLICANT: DOYLE, L. Austin
APPLICANT: ABRUZZO, Lynne
TITLE OF INVENTION: BEBAST CANCER RESISTANCE
TITLE OF INVENTION: WHICH ENCODES IT
FILE REFERENCE: EP19376-019
CURRENT FILIN UNUBER: US/09/961,086
CURRENT FILING DATE: 2001-09-21
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PRIOR APPLICATION NUMBER: US 60/073,763 PRIOR FILING DATE: 1998-02-05 PRIOR APPLICATION NUMBER: PCT/US99/02577 PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                         APPLICANT: UNIVERSITY OF MARYLAND,
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                                                                                                                                                                                                                     ROSS, Douglas D.
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Pred. No. 9.5e-54;
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US-09-961-086-1
                                                                                                                                                                                                                      Sequence 35, Application US/09981353 Patent No. US20020160382A1 GENERAL INFORMATION:
                               CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 35
LENGTH: 655
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1
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Best Local Similarity
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                                                                                                                                            APPLICANT: Lasek, Amy W. APPLICANT: Jones, David A. TITLE OF INVENTION: GENES ET FILE REFERENCE: PA-0038 US
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TYPE: PRT
                 TYPE: PRT
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Pred. No. 1.8e-52;
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GENERAL INFORMATION:

APPLICANT: MASSACHUSETTS GENERAL HOSPITAL

TITLE OF INVENTION: Stem Cells of the Islets

TITLE OF INVENTION: Mellitus

TITLE OF INVENTION: Mellitus

FILE REFERENCE: 3284/1235B

CURRENT APPLICATION NUMBER: US/10/120,687

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: US60/169082

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: US 60/963,875

PRIOR APPLICATION NUMBER: US 60/215109

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: US 60/238880
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US-10-120-687-61
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                                                                                                                                                                                                                                                                         Sequence 61, Application US/10120687 Publication No. US20030082155A1
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                                                                                                                                              Sequence 5, Application US/10090455 Publication No. US20030027259A1 GEMERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 61
                          APPLICANT: Chen, Hongyun
APPLICANT: Le Bihan, Stephane
TITLE OF INVENTION: NOVEL ABGG4 TRANSPORTER
FILE REFERENCE: 100103.406
CURRENT APPLICATION NUMBER: US/10/090,455
CURRENT FILING DATE: 2002-03-01
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     NUMBER OF
SOFTWARE:
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Pred. No. 2.7e-52;
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                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                    Sequence 10, Application US/09866866A Patent No. US20020102244A1
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Best Local Similarity
                                                                                                                                                       APPLICANT: Sorrentino, Brian
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating
FILE REFERENCE: 1340-1-021CIP2
               PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
                                                                                                                       CURRENT APPLICATION NUMBER: US/09/866,866A CURRENT FILING DATE: 2001-08-30
                                                                                     PRIOR APPLICATION NUMBER: 09/584,586 PRIOR FILING DATE: 2000-05-31
UMBER OF
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SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                    VSVTTNPMCAFTQGIQFIEKTCPG 615
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; ORGANISM: Homo sapien
US-09-866-866A-10
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                                                                                                                                                                                                                             Sequence 27, Application US/09866866A Patent No. US20020102244A1
                                                                                                                                                                                                                GENERAL INFORMATION
                                  CURRENT APPLICATION NUMBER: US/09/866,866A CURRENT FILING DATE: 2001-08-30 PRIOR APPLICATION NUMBER: 09/584,586 PRIOR FILING DATE: 2000-05-31 PRIOR APPLICATION NUMBER: PCT/US99/11825 PRIOR FILING DATE: 1999-05-27
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SEQ ID NO 10
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                                                                                                                                        APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying
FILE REFERENCE: 1340-1-021CIP2
                                                                                                                                                                              APPLICANT: Sorrentino, Brian APPLICANT: Schuetz, John
         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                       APPLICATION NUMBER: 60/086,988
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                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                       Sequence 14, Application US/09866866A Patent No. US20020102244A1
                                                                             APPLICANT: Sorrentino, Brian
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying
FILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
              PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
                                                PRIOR APPLICATION NUMBER: 09/584,586 PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 60/086,988
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SOFTWARE: PatentIn
SEQ ID NO 27
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Best Local
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TYPE: PRT
ORGANISM: Homo sapien
  595
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                                                                                TLLMTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPG---
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                                          VSVTTNPMCAFTQGIQFIEKTCPG 615
                                                                                                                          VALLSIAGV -- LVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSN 591
                                                                                                                                                                          MRMLPSIIFTCIVYFMLGLKAKADAFFVMMFTLM---MVAYSASSMALAIAAGQSVVSVA
                                                                                                                                                                                                                  FSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSV
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NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 657
TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                     570 YCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPG 615
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                                                                             YGFTALQYNEFLGQEFCPG---FNVTDNSTCVNSYAI-----CTG 612
                                                                                                                                                                                                                                                 YISGYYRVSSYFFGKVMSDLLPMRFLPSVIFTCILYFMLGLKKTVDAFFIMMFTLI---M
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Scoring table:
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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3326
1 MGDLSSLTPGGSMGLQVNRG......PALVILGIVVFKIRDHLISR 651
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Human ABCG5 protei
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Human ABCG5 mutant
Human ABCG5 mutant
Human ABCG5 mutant
Human ABCG5 mutant
Mouse sitosterolae
Mouse sitosterolae
Mouse ABCG5 protei
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13.9 812	14.2 689	15.5 832	16.6 666	17.0 616	17.1 666	17.2 609	17.3 653	.3 649	17.4 604	17.4 604	17.4 646	17.5 687	17.7 632	17.7 625	17.7 648	18.0 602	18.1 687	19.8 657	20.2 655	20.3 655	20.3 655	20.3 655	20.3 665	20.5 665	20.5 655	20.5 655	20.5 655	20.5 663	20.5 655	. 21.7 144	37.1 243	.5 41.7 340		7.5 82.0 652
								AAG43100														AAY95365						AAY15221				AAU969	AAUS	AAU9
Drosophila melanog				Arabidopsis thalia	Mouse ischaemic co	=	Arabidopsis thalia		Human polypeptide	Human secreted pro	ısı				S.		_	e BCRP	BCRP	BCRP	n BCRP/M	-	BCRP-	BCRP-	BCRP pro	ABCG2. H	transport p	t Cance	· ABCG2		CG5 mc	r ABCG	an ABCG	Rat ABCG5 protein.

ALIGNMENTS

Key Location/Qualifiers Misc-difference 2..15 Human; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease; chromosome 2p21. 25-SEP-2000; 2000US-235268P. Patel SB, (USSH) US DEPT HEALTH & HUMAN SERVICES. (PATE/) PATEL S B. (DEAN/) DEAN M. 25-SEP-2001; 2001WO-US29859 04-APR-2002. WO200227016-A2 Homo sapiens Dean M; /note- "Encoded by GGTCTC"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or mammal comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The ABCG5 biological activity, or level of ABCG5 mRNA, or level of the polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal to a mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a second cell culture or mammal tomprising a wild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present amino acid sequence is encoded by the human ABCG5 gene located on chromosome 2p21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel mammalian ATP-binding cassette gene 5 polypeptide, and nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
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IFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIA
                                                                                                GLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATM
                                                                                                                                                                            SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRV
                                                                                                                                                                                                                                                      YMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKD
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                                                                             GLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATM
                                                                                                                                                                                                                                     YMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKD
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                                                                                                                                                       SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRV
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Pred. No. 0
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Matches Query Match Best Local

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Similarity

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                                         The invention relates to an isolated Sitosterolaemia Susceptibility Gene (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) CC binding cassette (ABC) family cholesterol transporter. SSG is useful CC for identifying a compound useful in the treatment or prevention of a CC sterol-related disorder, including sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or CC nutritional deficiencies. SSG is also useful for treating cholesterol-associated diseases or conditions including coronary heart disease and CC cher cardiovascular diseases, and sitosterolaemia-associated condition CC including arthritis, xanthomas and chronic haemolytic anaemia. SSG CC expression cassette is useful in the production of transgenic non-human CC animals. SSG genes and their homologues are useful as tools for a number CC ardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The present sequence is human SSG protein. Human SSG is located on chromosome
                                                                                                                                                                                                                                                                                                                                                                Novel sitosterolemia susceptibility gene polypeptide and polynucleotide, useful for screening a compound that increases level of expression or activity of SSG polypeptide for treating sterol-related disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                 Claim 19; Fig 8; 105pp; English.
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15-MAY-2000;
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                                                                                                                                                                                            Human; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
                                                                                                                                                                                                                                 Human ABCG5 mutant E146Q protein sequence
                       25-SEP-2001; 2001WO-US29859
                                                04-APR-2002
                                                                        W0200227016-A2
                                                                                                             Misc-difference
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                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABGC5) polypeptide. The invention is useful for identifying a creatisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and cc measuring ABCG5 biological activity in the cell culture or in mammal, cwhere an increase or decrease in ABCG5 biological activity compared to CC ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or certain comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mutation of the compound that increases or CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC Polypeptide in a cell culture or mammal is also compared with that of a csecond cell culture or mammal is useful for treating or preventing construction of ABCG5 activity is useful for treating or preventing construction and/or decreasing cholesterol acid sequence represents the human ABCG5 mutant E146Q protein of the coveration.
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel mammalian ATP-binding cassette gene 5 polypeptide, a nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                       specification.
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SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLINGLFLLFFVLRVRSNVLKGAIQDRV
                                                  YMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLDMVPFKTKD
                                                                                    RNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDF
                                                                                                                                      ADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR
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                                                                                                                                                                                                                                                                                         MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSC
                                     YMDLTSYDTQSKEREIETSKRYQMIESAYKKSAICHKTLKNIERMKHLKTLPMYPFKTKD
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Pred. No. 0;
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            The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cel culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or
                                                                                                                                                                                                                                                                                                               Novel mammalian ATP-binding cassette gene 5 polypeptide, a nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                           Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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AAU96990 standard; Protein; 651

RESULT 5
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30-JUL-2002 (first entry)

Human ABCG5 mutant

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Mote: This sequence is not shown in the specification but is derived
from the wild-type human ABCG5 protein (AAU96984) given on pages 35-36
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Synthetic.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B. (DEAN/) DEAN M.
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                                                                                                                                                                                                    Homo sapiens Synthetic.
                                                                                                                                                                                                                                          mutant; mutein.
                                                                                                                                                                                                                                                  Human; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                             AAU96993;
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                                                   25-SEP-2000; 2000US-235268P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell CC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a GC contilation of ABCG5 activity is useful for treating or preventing CC hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's CC disease. The method of the invention is useful for increasing cholesterol acid securence represents the human ABCG5 mutant Rd19p protein of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel mammalian ATP-binding cassette gene 5 polypeptide, and nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
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IFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIA
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RESULT 7
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ID AAE1
 The invention relates to an isolated Sitosterolaemia Susceptibility Gene (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) CC binding cassette (ABC) family cholesterol transporter. SSG is useful CC for identifying a compound useful in the treatment or prevention of a CC sterol-related disorder, including sitosterolaemia, hyperlipidaemia, CC hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or CC nutritional deficiencies. SSG is also useful for treating cholesterol-CC associated diseases or conditions including coronary heart disease and CC other cardiovascular diseases, and sitosterolaemia-associated condition including arthritis, xanthomas and chronic haemolytic anaemia. SSG expression cassette is useful in the production of transgenic non-human CC animals. SSG genes and their homologues are useful as tools for a number CC of applications including diagnosing sitosterolaemia and other CC cardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The CC cardiovascular disorders, for forensics and paternity determinations, the control of treating any of a large number of SSG associated diseases. The CC cardiovascular disorders, for forensics and paternity determinations, and control of treating any of a large number of SSG associated diseases. The
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Note: The present
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                                                                                                                                                                                                                                                                                                                                                                Novel sitosterolemia susceptibility gene polypeptide and polynucleotide, useful for screening a compound that increases the level of expression or activity of SSG polypeptide for treating sterol-related disorder
                                                                                                                                                                                                                                                                                                                              Disclosure; Page -; 105pp;
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                                                                      Mouse; sitosterolaemia susceptibility gene; SSG; atherosclerosis; sterol-related disorder; hyperlipidaemia; hypercholesterolaemia; sterol-related disorder; disease; cardiovascular disease; arthritis; animal: chromosome 17; therapy.
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                                               Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide, useful for screening a compound that increases level of expression or activity of SSG polypeptide for treating sterol-related disorder
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                                     The invention relates to an isolated Sitosterolaemia Susceptibility Gene (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) binding cassette (ABC) family cholesterol transporter. SSG is useful for identifying a compound useful in the treatment or prevention of a sterol-related disorder, including sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or nutritional deficiencies. SSG is also useful for treating cholesterolaesociated diseases or conditions including coronary heart disease and associated diseases or conditions including coronary heart disease and
   other cardiovascular diseases, and sitosterolaemia-associated of including arthritis, xanthomas and chronic haemolytic anaemia. expression cassette is useful in the production of transgenic respectively.
                                                                                                                                                                            Novel sitosterolemia susceptibility gene polypeptide polynucleotide, useful for screening a compound that level of expression or activity of SSG polypeptide for
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                                                                                       CAFTQGIQFIEKTCPGATSRFTMNFLILYSFIPALVILGIVVFKIRDHLISR
                                          SGLLIGSGFIRNIQEMPIPLKILGYFTFQKYCCEILVVNEFYGLNFTCGGSNTSMLNHPM
                                                      AGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSYTTNPM
                                                                                                                                                 VGLLYQFYGATPYTGMLNAVNLFPYLRAVSDQESQDGLYQKWQMMLAYALHYLPFSVVAT
                                                                                                                                                                                          DSPGVESKLGVLLRRYTRNLVRNKLAVITRLLQNLIMGLELLEEVLRVRSNVLKGAIQDR
                                                                                                                                                                                                                                         FYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTK
                                                                                                                                                                                                                                                                       LRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEP-HSLGILHASYSVSHRVRPWWDITS
                                                                                                                                                                                DPPGMFGKLGVLLRRVTRNLMRNKQAVIMRLVQNLIMGLFLIFYLLRVQNNTLKGAVQDR
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                                                                                                                                                                                                                                                                                                                                                                LRRDQFQDCFSYVLQSDVFLSSLTVRETLRYTAMLALCRSSADFYNKKVEAVMTELSLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGELPFLSPEGARGPHLNRGSLSSLEQGSVTGTEARHSLGVLHVSYSVSNRVGPWWNIKS
                                                                                                                                     VGLLYQLVGATPYTGMLNAVNLFPMLRAVSDQESQDGLYHKWQMLLAYVLHVLPFSVIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     652 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing sitosterolaemia and other for forensics and paternity determinations, large number of SSG associated diseases. The SSG protein variant obtained by replacing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2742.5; DB 2
Pred. No. 4.7e-280;
4; Mismatches 64;
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SEQ
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ID NO: 1 (AAE13289
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RESULT 10
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ID AAU966
XX AAU96
AC AAU96
XC AAU96
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XX MOUS6
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           arteriosclerosis;
                                                              30-JUL-2002
                                                                                                     AAU96985
                     Mouse;
                                          Mouse ABCG5
                                                                                  AAU96985
                     ABCG5;
                                                                                                     standard;
                                        protein.
     ATP-binding casser, heart disease;
                                                                                                     Protein;
                                                            entry)
       cassette gene 5; sitost
isease; hypersterolemia;
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                  sitosterolemia;
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Alzheimer's

cholesterol;

disease.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                  CRQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRA 119
                                                                                                                                                      LRREOFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSH 179
        RRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFD
                                            LRRDQFQDCFSYVLQSDVFLSSLTVRETLRYTAMLALCRSSADFYNKKVEAVMTELSLSH
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                                                                                                                                                                                                                                                                                                                                                                                             82.3%; Score 2738.5; DB 2:
80.1%; Pred. No. 1.2e-279;
Live 64; Mismatches 65;
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RESULT 11
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D96986
AAU96986 standard; Protein; 652 AA.

AAU96986;
30-JUL-2002 (first entry)
Rat ABCG5 protein.
Rat; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterolarteriosclerosis; heart disease; hypersterolemia; Alzheimer's diseas Rat sp.

WO200227016-A2.

04-APR-2002.

25-SEP-2001; 2001WO-US29859

25-SEP-2000; 2000US-235268P

(USSH) US DEPT HEALTH & HUMAN SERVICES. (PATE/) PATEL S B. (DEAN/) DEAN M.

Patel SB, Dean M;
WPI; 2002-416483/44.
N-PSDB; ABK51686.

Novel mammalian ATP-binding cassette gene 5 polypeptide, and the nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases

Example 3; Page 45; 66pp; English.

CC The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying CC a compound which alters ABCG5 activity level comprising contacting a cel culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal,

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RESULT 12
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Best Local S
Matches 518
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                30-JUL-2002
                                                AAU96991;
                                                                            AAU96991 standard; Protein;
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79.4%;
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SS X

Sequence

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Query Match Best Local : Matches

408;

Similarity

62.6%; llarity 100.0%; Conservative

Score 2081; DB 23; pred. No. 1.7e-210; 0; Mismatches 0;

Length Indels

408;

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Gaps

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The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, asteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell CC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal. CC where an increase or decrease in ABCG5 biological activity on a control cell culture or mammal not CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC ABCG5 biological activity respectively. The cell culture or mammal CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity or level of ABCG5 mRNA, or level of the CC ABCG5 biological activity is useful for treating or preventing CC hypertide in a cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a CC scond cell culture or mammal is also compared with that of a CC polypeptide in a cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a ceromatic compared compared with that of a ceromatic compared compared with that of a ceromatic compared compared with that of a ceromatic compared compared with that of a ceromatic compared compared with that of a ceromatic compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compare
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of the specification.
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                    Note: This sequence is not shown in the specification but is derived from the wild-type human ABCG5 protein (AAU96984) given on pages 35-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B.
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           The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and measuring ABCG5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCG5 biological activity compared to ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or mammal comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The approved that increases are compound that increases are compounded and the activity respectively.
                                                                                                                                                                                                                                                                                                           Novel mammalian ATP-binding cassette gene 5 polypeptide, a nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
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N-PSDB; ABK51687.
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                                                                                                                                                                                                                                                                           Example 3; Page 46; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES (PATE/) PATEL S B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVR 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDF 300
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Best Local
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Patel SB,
                                                                                                                                                                                           04-APR-2002.
                                                                                                                                                                                                                               W0200227016-A2
                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                       mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU96988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU96988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                         mutein.
Dean
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polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal comprising a wild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present amino acid sequence represents the hamster ABCG5 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 AMSGRIGRAGTFIGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                        LFLLFEVLRVRSNVLKGAIQDRVGLLYQFVGATPYT
                                                                                                                                                                 LFLIFYLLRVQNDILKGAIQDRVGLLYSW-SAPPRT
                                                                                  TLKNIERMKHLKTLPMYPEKTKDSPGYESKLGYLLRRYTRNLYRNKLAVITRLLQNLIMG
                                                                                                                                                                                                                                                      EPTTGLDCMTANQIVILLAELARRDRIVIVTIHQPRSELFQHFDKIAILTYGEMVFCGTP
                                                                                                                                                                                                                                                                       EPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTP
                                                                                                                                                                                                                                                                                                                                          SSSSDFYDKKVEAVMEELSLSHVADRMIGNYNFGGISSGERRRVSIAAQLIQDPKIMMFD
                                                                                                                                                                                                                                                                                                                                                                                                                              AISGRLRRTGTLEGEVEVNGRELRRDQFQDCFSYVLQSDVFLSSLTVRETLRYTAMLALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.78; 78.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1387.5; DB 23; Pred. No. 2.2e-137; 9; Mismatches 32;
                                          433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                           337
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T 14.

3988

AAU96988 standard; Protein; 243 AA.

AAU96988;

30-JUL-2002 (first entry)

Human ABCG5 mutant R243X protein sequence.

Human; ABCG5; ATP-binding cassette gene 5; sitosterolemia; chol arteriosclerosis; heart disease; hypersterolemia; Alzheimer's d mutant; mutein.
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Homo sapiens.

Synthetic.

Location/Qualifiers

Key
Misc-difference 243

/note= "Wild-type protein truncated at this position"

WO200227016-A2.

04-APR-2002.

25-SEP-2001; 2001WO-US29859.

25-SEP-2000; 2000US-235268P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

(PATE/) PATEL S B.

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AAB41856
ID AAB4
XX
AC AAB4
XX
AC AAB4
XX
DT 08-F
DT 08-F
DX
DX
Huma
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Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Culture or mammal which have ABCG5 polypeptide with a compound and characteristic where an increase or decrease in ABCG5 biological activity in the cell culture or in mammal, which have ABCG5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or contacted with the compound, identifies a compound that increases or contacted with the compound, identifies a compound that increases or comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The cell control contacted in a cell culture or mammal is also compared with that of a compound that increases or conjugate in a cell culture or mammal is also compared with that of a conjugate in a cell culture or mammal is also compared with that of a conjugate in a cell culture or mammal is also compared with that of a conjugate in a cell culture or mammal comprising a wild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing conjugate. The method of the invention is useful for increasing cholesterol acid sequence represents the human ABCG5 mutant R243X protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                          Human ORFX ORF1620 polypeptide sequence
                                                                                  08-FEB-2001
                                                                                                                      AAB41856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a predisposition for developing situsterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABGG5 activity level comprising contacting a cell
                                                                                                                                                  AAB41856 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel mammalian ATP-binding cassette gene 5 polypeptide, and the nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page -; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-416483/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : This sequence is not shown in the specification but is derived the wild-type human ABCG5 protein (AAU96984) given on pages 35-
                                                                                                                                                                                                                                        241
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                  RQOWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRAL 120
                                                                                                                                                                                                                                        RNR
                                                                                                                                                                                                                                                                                                  ADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR
                                                                                                                                                                                                                                                                       RNR 243
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                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1234; DB 23;
Pred. No. 2.1e-121;
                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein (AAU96984) given on pages 35-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                          SEQ
                                            ID NO:3240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Human; open reading frame; ORFX; detection; vulnerary; antipsoriatic; antiparkinsonian;

cytostatic; hepatotropic; nootropic; neuroprotective;

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417

KTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAI 416

QDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSV

Matches

Similarity

0;

Mismatches

Indels

0,

240

180 180

60

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Query Match
Best Local
                                                                                                                                                          immunostinulant; cardiant; thrombolytic; coagulant; vasotropic; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allorates.
                                                                                                  allergies, aplastic anaemia, burns, wounds, bone and cartilage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                            which represent the human OREX open reading frames 1 to 3161. The OREX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 2444; 5507pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antingal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotre; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-602362/57.
                                                                144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0127636
99US-0127728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0127607
21.7%;
Score 722; DB 21;
Pred. No. 1.1e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                             to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS;
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Page 13

Qy Db Search completed: June 11, 2003, 09:12:15 Job time: 43 secs 61 QDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSV 120

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                    Score
                                                                                                  Match
                                                                                                                   Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    July 26, 2003, 23:50:29 ; Search time 4351.59 Seconds (without alignments) 13069.363 Million cell updates/sec
                     23.2
22.3
20.4
19.8
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                            Xu,X., Huang,J., Xú,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li.N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 594)
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AV689089 GKC Homo sapiens CDNA clone GKCDZB07 5', mRNA sequence.

AV689089 GI:10290952
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T93792 ye05f01.sl
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AA012016 mx02d10.r
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AA0502855 BX092855
AA237183 mx17f01.rl
AA05038 Mus muscu
CD502117 CDA54-H04
CB813243 AMGNNUC:T
CB812866 AMGNNUC:T
CB812866 AMGNNUC:T
CB812753 Pan trogl
BF620684 HVSMEc002
BM725726 UI-E-EJU-
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BF162656 601769307

BY742680 BY742680

AV695922 AV695922

BMB56449 K-EST0140

AV669973 AV660973
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           Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Email: hanzg@chgc.sh.cn
This clone is available
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/mol_type="mRNA"
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/dev_stage="Adult"
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/clone="GKCDZB07"
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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201203, P. R. China
Tel: 86-21-50801919(ex.45)
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This clone is available at CHGC
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Chinese National
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                                                        ACTTGGTATCGTCCAAAATCCAAATATAGTCAACAGTGTAGTGGCTCTGCTGTGTGCATTGC
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/dev_stage="Adult"
/lab_host="SOLR"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AV720911/c
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351 Guo Shoujing Road, Zhangjiang
201203, P. R. China
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Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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Contact: Zec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 477)
     CTTGGATCCAAGCAGGCCTTGAATGCAATGGAAGTGGTTTATAGTCCCTTGCTCTTACAA 2262
                                Homo sapiens cDNA GLC clones
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                                                                                                                                                         AGTTGTTTTCAAAATAAGGGATCATCTCATTAGCAGGTAGTGAAAGGCCATGGCTGGGAAA 2082
                                                                                                                                                                                                                           ATTCACAATGAACTTTCTGATTTTGTATTCATTTATTCCAGCTCTTGTCATCCTAGGAAT
                                                                                                                                                                                                                                                      GTGTGCCTTCACTCAAGGAATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAG
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                                                                                        ### ATGGAAGTGAAGCTGCCGACTGTGCATGACTCTGAAACGTCTGAAATGAGAGTGCCAT
                                                                                                                                           AGTTGTTTTCAAAATAAGGGATCATCTCATTAGCAGGTAGTGAAAGCCATGGCTGGGAAA
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                                                                                                                                                                                                                                                                                                                         GTTCTACGGACTGAATTTCACTTGTGGCAGCTCAAATGTTTCTGTGACAACTAATCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l: hanzg@chgc.sh.cn
clone is available at CHGC
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCETC06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="GLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
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100.0%; Pr
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Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
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Pred. No. 6.1e-112;
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BB598373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81-45-503-9216
/organism="Mus musculus"
/mol_type="mRNA"
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                Contact: Yoshihide Hayashizaki
                                                                                                Unpublished On Dec 1, 2000 this sequence version replaced gi:11506974.
                                                                                                                                            RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                               1 (bases 1 to 713)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
          1-7-22 Suehiro-cho,
                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                               , Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., K., M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sa, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.
                                                                                                                                                                                                                                                                                                                                                                                                           BB598373.2 GI:16450340 EST.
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                                                                                                                                                                Tagawa, A., Takahashi, F., M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                   Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
      Tsurumi-ku,
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      Yokohama,
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    Kanagawa
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230-0045, Japan
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                                                                                                                                                                               Toya, T.,
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prepare full-length cDNA libraries for rapid discovery of genes. Genome Res. 10 (10), 1617-1630 (2000) wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohal Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayasi Addition, Shibata, F., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to CDNAS

,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Hayashizaki,Y. Kira, A. Ohara,E., T., Matsuura

sequencing pipeline with 384 multicapillary 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M. Y. and Hayashizaki,Y Shibata, K., Itoh, M., Carninci, P., sequencer. Genome Res. Sugahara

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

Please visit our web site (http://genome.gsc.rlken.go.jp/) for further details. Human Genome Sequences Mamm. Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences Mamm. Genome. 12, 673-677 (2001)

prepare mouse tissues Division of Experimental Animal Encyclopedia Project of Genome Exploration Genomic Sciences Center and Genome Science cDNA library was prepared and sequenced in Mouse Genome Location/Qualifiers in Research Group in Riken Laboratory in RIKEN.

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CTCACATCAACAGAGGGTCTCTGAGCTCCCTGGAGCAAGGTTCGGTCACGGGCACAGAGG
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                                                          TGGCCATCCGCCGCGCAATCCCCGGCTCCTTCCAGAAGAAGGTGGAGGCCGTCATGGCAG
                                                                                                                                        AGAGCGACACCCTGCTGAGCAGCCTCACCGTGCGAGACGCTGCACTACACCGCGCTGC
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                                       TGGCCCTCTGCCGCAGCTCCGCGGACTTCTACAACAAGAAGGTAGAGGCAGTCATGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                    TGTACGTGGAGAGCGGGCAGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAAAACCA
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AGCTGAGTCTGAGCCATGTGGCAGACCGACTGATTGGCAACTACAGCTTGGGGGGCATTT
                                                                                                                   AGAGCGACGTTTTTCTGAGCAGCCTCACTGTGCGCGAGACGTTGCGATACACAGCGATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host-"DH10B"
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/clone="C730003G04"
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               2028 TTTTCAAAATAAGGGATCATCTCATTAGCAGGTAGTGAAAGCCATGGCTGGGAAAATGGA 2087
                                                                                                                                                         1908 CCTTCACTCAAGGAATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAGATTCA
                                                                                           1968 CAATGAACTTTCTGATTTTGTATTCATTTATTCCAGCTCTTGTCATCCTAGGAATAGTTG
                                                           372 CAATGAACTTTCTGATTTTGTATTCATTTATTCCAGCTCTTGTCATCCTAGGAATAGTTG
                                                                                                                            432 CCTTCACTCAAGGAATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAGATTCA
 312 TTTTCAAAATAAGGGATCATCTCATTAGCAGGTAGTGAAAGCCATGGCTGGGAAAATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 364.
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                                                                                                                                                                                                                                                                                                                                                 (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                          constructed by Bento Soares and M.Fatima Bonaldo. 89 c 85~g 126~t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                       (Pharmacia), digested with Pac I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="20 week-post conception fetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1655179"
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                                                                                                                                                                                                          18.3%;
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                                                                                                                                                                                                          Score 429;
Pred. No.
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                                                                                                                                                                                             Mismatches
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1.5e-99;
                                                                                                                                                                                                                         Length 432
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                        Matches 418;
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qe21a04.x1 Soares_fetal_lung_NbHL19W
IMAGE:1739598 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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h quality sequence stop: 417.
Location/Qualifiers
                      Conservative
                                                                                                                             sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Index
                                                                                                    Soares and M.Fatima Bonaldo. This libra from the same fetus as the fetal heart foral heart NhHH19W "
                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:1739598"
/dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                 /mol_type-"mRNA"
                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                17.9%;
100.0%; Pr
0;
                                                                                    heart NbHH19W.
39 c 80 g
                   Score 418; DE
; Pred. No. 1e-
0; Mismatches
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                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9197 row: m column: 02
                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, ph.D.
                                                                                                                                                                                                                       High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                             NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601769307F1 NCI_CGAP_Lu29
                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                (bases
           245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
/Clone_lib="NCI_CGAP_Lu29"
/note="organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note="organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned uniddrectionally. Primer: Oligo (
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH*

248 c 257 g 185 t 1 others
                                                                                                   /tissue_type="spontaneous tumor, metastatic
Stem cell origin."
                                                                                      /lab_host="DH10B"
                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:3988777"
                                                                                                                                                       /mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                 1. .936
                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             1 to 936)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:11042879
                                                                                                                                                                                                                      row: m column:
|uence stop: 686.
                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; ¡
Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               936 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus
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RESULT 8
BY742680
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                                                                                                                                                                                                                                                                                                                                                                        musculus
BY742680
                    Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyo, Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batal, C., Chang, M., Marsuda, H., Batal, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chan
                                                                                                                                   Okazaki,Y., Furuno,M.,
                                                                                                                                                                                                                                                                                                                                                                                   BY742680 RIKEN full-length enriched, adult male l musculus cDNA clone C730040P06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY742680
                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                     Mus
                                                                                                                                                                                                                                                                                                                                        BY742680.1 GI:27168376
     Beisel,K.W., Blake,J.A., Bradt,D.,
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                                                                                                                                                                        (bases 1 to 658)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAAACTGGGTGTTCTCCTGAGGAGAGTGACAAGAAACT--TGGTGAGAAATAAGCTGGC 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATACCTGAAAACCTTAACCACGGTTCCTTTCAAAACAAAAAGATCTCCTGGGATGTTCG 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGCCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAG--AATATTGAAAGAATGA 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGACACCCAAAGCAGAGAGCGGGAAATAGAAACGTACAAGCGAGTACAGATGCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGGATAAATGCGCCACGGCAGAACTCGGTCACGGGCCTTCACCACATAT: 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTT 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAGCTTGGGGTCCTGGAGAGGGAATTACAAGAAACCTCCACGCGCGAATAAGCACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGATACCCAAAGCAAGGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGATAGAA 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTTACGGAGAGTNGGTGTTCTGTGGCACCCCAGAGGAGGTGCTTGGCTTCTTCAATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCACCATCCACCAGCCTCGCTCTGAGCTCTTCCAACACTTCGACAAAATTGCCATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCACCATTCACCAGCCCCGTTCTGAGCTTTTTCAGCTCTTTGACAAAATTGCCATCCTG
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                                                                                                                                                                                                                                                        musculus
                                                                                                                                                                                                                                                                            musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                               Eutheria; Rodentia;
                                                                                                                                                                                                                            Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.4%;
75.2%;
                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 8.2e-94;
                                                                                                                                      Kasukawa, T., Adachi, J., Bono, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               658 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
Brusic, V., Chothia, C., Corbani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                  adult male liver tumor Mus
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                                                                                                                                                                                               Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                               Batalov,S.
                                                                                                            Kiyosawa, H.
                                                                                                                                         Kondo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         844
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MEDLINE
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Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ringy
,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou
,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale
,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y.,
Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa
,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura
,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
,Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,J., Kawai,J., Kojima,Y., Kondo,S., Konno
,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.
Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm Carlton Streets, Buffalo, NY 14263, whose assistance we grati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp)
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: 81-45-503-9222
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                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="liver tumor"
/dev_stage="adult"
                                                                   /sex="male"
                                                                                                               /clone="C730040P06"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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d,T., Gariboldi,M., Gissi,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                  assistance we gratefully
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                                                CCACGGGTGAGCGGCCCGGGTCTCCATCGCAGCCAGCTGCTCCAGGATCCTAAG 742
                                                                                                                                                                TGGCCATCCGCCGCGCATCCCGGCTCCTTCCAGAAGAAGGTGGAGGCCGTCATGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male liver
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0; Mismatches 138;
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hanzg@chgc.sh.cn
This clone is available at CHGC
Location/Qualifiers
1.417
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                                                                                  GTGGCAGATGATGCTGGCCTATGCACTGCACGTCCTCCCCTTCAGCGTTGTTGCCACCAT 1545
                                                                                                                                     TCTGTTTCCCGTGCTGCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGAA 1485
                                                                                                                                                                                                       AGGTCTCCTTTACCAGTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAAĆGCTGTGAA 1425
                                                                                                                                                                                                                                                                                             CCTTTTCTTCGTTCTGCGGGTCCGAAGCAATGTGCTAAAGGGTGCTATCCAGGACCGCGT 1365
                                                                                                                                                                                                                                                                                                                                               GAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="hepatocellular carcinoma
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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/clone="GKCDWE04"
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                                                               2036 ATAAGGGATCATCTCATTAGCAGGTAGTGAAAGCCATGGCTGGGAAAATGGAAGTGAAGC
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                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: yongsung@mail.kribb.re.kr
Plate: 48 row: E column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 471)
Kim, N.S., Hahn, Y.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                         TTTCTGATTTTGTATTCATTTATTCCAGCTCTTGTCATCCTAGGAATAGTTGTTTTCAAA 2035
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Location/Qualifiers
                                                                                                                                                                                 15.6%; Score 365; DB 12; llarity 100.0%; Pred. No. 5.5e-83; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was
                                                                                                                                                                                                                                                                           converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coll Top10F' by electroporation method The cDNA libraries constructed by this method are full-length enriched cDNA library."

79 c 101 g 153 t
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/note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoR1;
/note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoR1;
Site_2: Not1; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
                                                                                                                                                                                                                                                                                                                                                                                          circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA str
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/mol_type="mRNA"
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV660973 GLC Homo sapiens cDNA clone GLCGNC08 AV660973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV660973.1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                 /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCGNC08"
                                                                                                                                                                                                         /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                   /clone_lib="GLC"
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                               Score 360; DB 9;
Pred. No. 9.5e-82;
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                                                                             Mismatches
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linear EST 16-JAN-2 108 3', mRNA sequence.

EST 16-JAN-2002

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RESULT 12
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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CA316999.1 GI:24535123
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1 (bases 1 to 794)
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE: 6811377"
//tissue_type="whole brain"
//tissue_type="whole brain"
//dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
//lab_host="NHIB (TI phage resistant)"
/clone_11b="NHH_BNAP_FWO"
/note="Organ: Brain; Vector: pXY- Asc; Site_1: Ecor I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institutes of Health, Mammalian
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/strain="C57BL/6"
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a 239 c 220 g
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AI597378
vj29c06.yl Stratagene mouse diaphragm (#937303) Mus clone IMAGE:930442 5', mRNA sequence.
AI597378 Mus musculus (house mouse) ; Chordata; ; Rodentia; Kucaba, T., Martin, J., Craniata; Vertebrata; Sciurognathi; Muridae Muridae; Beck, C., Euteleostomi; musculus EST 21-APR-1999 Wylie, T., Murinae;

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The WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/WashU-NCI Mouse EST Project 1999
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/note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
prepared from diaphragm muscle. Primer: Oligo dr. Average
insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTT 3'"
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/dev_stage="adult"
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA656720
424 bp mRNA linear EST 04-NOV-19-vp95e08.rl Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1092518 5' similar to SW:SCRT_DROME P45843 SCARLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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12.7%; Score 297; DB 14; Length 336; y 96.9%; Pred. No. 1.8e-65; rvative 0; Mismatches 8; Indels 2; Gaps	/organism="Homo sapiens" /db_xref="GDB:472474" /db_xref="CDB:472474" /db_xref="Laxon:9606" /clone="IMAGE:116857" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH108 (ampiclilin resistant)" /clone_1ib="Soares fetal liver spleen lNFLS" /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I = oligo(dT) primer lst strand cDNA was primed with a Pac I = oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTT	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 768 High quality sequence stops: 265 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information. Insert Length: 768 Std Error: 0.00 Seq primer: -21m13 High quality sequence stop: 265. Location/Qualifiers 1. 336	T93792.1 GI:726965 EST: EST: Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 336) Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J. Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Watterston The WashU-Merck EST Project Onpublished Contact willow by	GTGGCAGATGTGCTCCCCTACAGGTCATCAGGTTACAGAGTTTACAGGTTACAGAAGTTTACAGCAGATTTAGAACTTTACAGCAGATTTAGAACTTTACAGCAGATTTAGAACTTTACAGAAAGTTTAGAACTTTAGAACTTTAGAAAGTTTAGAAAGTTTAGAAAGTTTAGAAAATTAGAACAAAAAAAA	GTGGCAGATGATGCTGGCCTATGCACTGCACGTCCCCCTTCAGCCTTGTTGCCACCAT 1545

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APPLICANT: ADYUZZO, Lynne V.
APPLICANT: ROSS, Douglas D.
TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which
TITLE OF INVENTION: Horset Cancer Resistance Protein (BCRP) and DNA which
TITLE OF INVENTION: Horset Cancer Resistance Protein (BCRP) and DNA which
TITLE OF INVENTION: Horset Cancer Resistance Protein (BCRP) and DNA which
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/073763
EARLIER FILING DATE: 1998-02-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
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%; Pred. No. 1.96
138; Mismatches
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US-08-951-912-4
US-09-174-077-4
US-09-425-453A-6
US-09-425-453A-12
US-09-425-453A-20
US-09-134-001C-3215
US-08-936-644-2
US-08-9352-552-2
US-08-136-742A-2
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US-09-256-703-2

US-07-637-621-2

US-08-951-912-2

US-08-681-838A-2

US-08-681-838A-3

US-09-174-077-2

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: Sequence 3731, Application US/09134001C

: Patent No. 6380370
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US-09-134-001C-3731
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                                                        Sequence 2, Application Patent No. 5994088
GENERAL INFORMATION:
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Best Local Similarity 29.3
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3731
LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                      APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B
        TITLE
                                                                                                                                                                                                     190
                                                                                                                                                                                                                                                                                                          180 VADRLIGNYSIGGISTGERRRVSIAAQLIQDPKVMLFDEPTTGLDCMTANQIVVLLVELA 239
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        OF INVENTION:
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                                                                                                                                                                                           DEGMTMVIVTHEMRFAK-EVSNQIAFIHEGVIAEQGTPE---DIFN---HPKTEELQRF 241
                                                                                                                                                                                                                             RRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPF 298
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                                                                                                                                                                                                                                                                      VKDQ---RPHALSG----GQQQRVAIARALAMNPKVMLFDEPTSALDPELVNDVLKVIKELA
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                                                                                                   Application US/08752447
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Methods and Reagents for Preparing
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NAME: NO. 5994088nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 15-NOT CLASSIFICATION: 43
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          SRLAVITQNIANLGTGIIISFIYGWQLTLLLLAI--VPIIAIAGVVEMKMFAGQALKDKK
                                                                                                                                                              FVVGVFCAIINGGLQPAFAIIFSKIIGVFTRIDDPETKRQNSNLFSLLFLALGIISFITF
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15-NOV-1996
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                                                                                                                           -----LFLLFEVLRVRSNV-----
                                              -GLLYQFVGATPYTGMLNAVNLFPVL----
                                                                                                                                                                                                     ---VFSK-LGVLLR-----RVTRN-----LVRNKLAVITR 389
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Gaps

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158 490

Query Match Best Local Similarity 20.7%; pred. No. 1.5e-16; Matches 153; Conservative 106; Mismatches 229; Indels 250; Gaps 32; Qy 41 LHASYSVSHRVRPWWDITSCRQQWTROILKDVSLYVESGQIWCILGSSGSGKTTLLDAMS 100	FILING DATE: 15-ROV-1996 PATION NOMBER: 00/02/44/ PATION NO. 6365357nan, Kevin E REGISTRATION NUMBER: 35,303 REFERENCE/DOCKET NUMBER: 95,1121 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0808 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1280 amino acids TYPE: amino acids TOPOLOGY: 11near MOLECULE TYPE: protein US-09-316-167-2	EADABLE FORM: EADABLE FORM: IBM PC Compatible S YSTEM: PC-DOS/MS: Patentin Release PLICATION DATA: TON NUMBER: US/09/: PATEON CATION: CATION DATA: CATION DATA: CATION DATA:	US-09-316-167-2 ; Sequence 2, Application US/09316167 ; Patent No. 6365357 ; Patent No. 6365357 ; Patent No. 6365357 ; GENERAL INFORMATION: APPLICANT: Mechetner, Eugene APPLICANT: Mechetner, Eugene ITILE OF INVENTION: Methods and Reagents for Preparing and TITLE OF INVENTION: Using Immunoligeal Agents Specific for P-glycoprotein NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSE: McDonnell Boehnen Hulbert & Berghoff Ltd. STREET: 300 South Wacker Drive, Seventh Floor CITY: Chicago STATE: Illinois COUNTRY: USA	
YTRY: 94 1ER H UTER H UTER WATIN WARE T AFI ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICA	RESULT 5 US-08-784-649A-2 Sequence 2, Application US/08784649A Patent No. 5830697 GENERAL INFORMATION: APPLICANT: Sikic, Branimir I APPLICANT: Chen, Gang TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO TITLE OF INVENTION: CYCLOSPORIN MODULATION NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 200 Sand Hill Road STATE: CA	OY 481 IFSVCYMPIGLHPEVAREYFSAALAPHLIGEY-LITURGIQUPNIVNSV533 1	711 390 771 418 831 453 889	GERRRYSIAAQLLQDP ::: :: ::: GCKORIAIARALVRNP LEQLFDKIAILSFGEL :TVRNADVIAGFDDGVI LETSK

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         RESULT 6
US-08-583-276-19
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
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LENGTH: 1279 amino acids
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STRANDEDNESS: si
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REFERENCE/DOCKET NUMBER: 06037/007001
                                                                             040 VENYPTRPDIPVLQGL 1055
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                                                                                                               NVSVTTNPMCAFTQGI 606
                                                                                                                                              DYAKAKISAAHIIM-----IIEKTPL-----
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                                                                                                                                                                                                                   FSYAGCF-----RFG----AYLVAHKLMSFEDVLLVFSAVVFGAMAVGQVSSFAP
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Pred. No. 4e-16;
08; Mismatches 230; Indels 246;
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Best Local :
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SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 05-JAN-1996
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PRIOR APPLICATION DATA:
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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New Jersey
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VGVFCAIINGGLQPAFAIIFSKIIGVFTRIDDPETKRQNSNLFSLLFLALGIISFITFFL 772
                                                                                                         MIESAYKKSAICHKTLKNIERMKHL-----
                                                                                                                                                                          IFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETS-----KRVQ
                                                                                                                                                                                                              KILLLDEATSALD-TESEAVVQVALDKARKGRTTIVIAH--RLSTVRNADVIAGFDDGVI 606
                                                                                                                                                                                                                                               KVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGEL 271
                                                                                                                                                                                                                                                                                GRQNVTMDEIEKAVKEANAYDFIMKLPHKFDTLVGERG-AQLSGGQKQRIAIARALVRNP
                                                                  MSSNDSRSSLIRKRSTRRSVRGSQAQDRKLSTKEALDESIPPVSFWRIMKLNLTEWPYFV 712
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                                 ------VFSK-LGVLLR-----RVTRN-----LVRNKLAVITRLL 391
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MULTIDRUG RESISTANCE GENES AND IMPROVED
SELECTION OF CELLS TRANSDUCED WITH SUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.7%;
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Pred. No. 4e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 1280;
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                                                                                                      --KTLPMVPF-----KTKDSPG--
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Gaps

363 652 323 549

Db 491 GRENVTWDEIEKAVKEANAYDETMKLPHKFDTLVGERG - AQLSGGOKQRIAIARALVRNP 549 212 KVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFOKIAILSFGEL 271 Db 550 KILLLDEATSALD-TESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAGFDDGVI 606 Qy 272 IFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKERBIETSKRVQ 323	6; Length 6; Inde 230; Inde 230; Inde xvesqqimcii - -	RESULT 7 \$206352-4 \$206352-4 \$206352-4 \$206352-4 \$206352-4 \$206352-4 Replicant: Roninson, Igor B.; Pastan Ira H.; Gottesman, Michael M. #ITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA SEQUENCES APPLICATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS **UNMBER OF SEQUENCES: 4 **CURRENT APPLICATION UNUMBER: US/07/622,836 ### FILING DATE: 24-SEP-1990 **PRICA APPLICATION NUMBER: 892,575 ### APPLICATION NUMBER: 892,575 ### FILING DATE: 01-AUG-1986 ### APPLICATION NUMBER: 845,610 ### FILING DATE: 28-MAR-1986 **SEQ ID NO:4: LENGTH: 1280	QY 392 QNLIMGLELLFEYLRYRSNYLKGAIQDR 419
INTEGRATION INTEGR	ADDRESSEE: GENZYME CORPORATION STREET: One Mountain Road CITY: Framingham STATE: Massachusetts COUNTRY: United States of America ZIP: 01701 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/665,259 FILING DATE: 17-JUN-1996	Qy 591 NVSVTTNPMCAFTQGI 606 Db 1041 VENYPTRPDIPVLQGL 1056 RESULT 8	Qy 364

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                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                          REFERENCE/DOCKET NUMBER: IG
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
MOLECULE TYPE:
                                                                                                                                                                                                                                                                          FILING DATE: 17-JUN-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/665,259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
                                                                                                                                                                           NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0
FILING DATE: 09-DEC-1996
                                                  LENGTH:
                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 TIVLTTHE-MDEADLLGDRIAIMAKGELQCCGSSLFLKQKYG-AGYHMTLVKEPHCNPED 752
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                                                1684 amino acids
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                                                                                                                            (508)
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                                                                                                                                                                                                                                       17-JUN-1996
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32.5%;
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METHODS OF MAKING AND USING SAME
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RESULT 10
US-08-762-500-75
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                                                                                   TELEFAX: (508)
INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 00 FILING DATE: 17-JUN-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
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MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                       REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01
FILING DATE: 09-DEC-1996
                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                              1704 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Connors, Timothy D.
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                                                                                                                         (508)
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                                                                                                                                                                                                                             17-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOSITIONS, METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.30
                                                                                                                                                                                                                                              PCT/US96/10469
                                                                                                                                                                                                                                                                                                                                                                        US/08/762,500
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Pred. No. 7.:
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILLING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILLING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3832
LENGTH: 242
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US-09-134-001C-3832
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        Sequence 3369, Application Patent No. 6380370 GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Staphylococcus epidermidis -09-134-001C-3832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUSTITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2.
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                      233 RTENF 237
                                                                                                                                                                                     182
                                                                                                                                                                                                          236 VELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHS 295
                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                       176 SLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLL
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                                                                                                                                                      NPFDF 300
                                                                                                                                                                                RQLANESMTMVIVTHE-MNFAKEISDKVVFMADGVVVESGTPQNI-
                                                                                                                                                                                                                                                                                                                                                                          EVLRDINLTVEKGEVVAIIGPSGSGKSTLLRCMN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --WNSRSRFLSGGMRRKLSIGIALIAGSKVLILDEPTSGMDAISRRAIWDLL-QRQKSDR
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Pred. No. 2.3e-16;
6; Mismatches 90
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Pred. No. 7.5e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100;
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US-08-395-246C-2
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08395246C Patent No. 5773214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3369
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APPLICANT: Skatru
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TYPE: PRT
                                                            CURRENT APPLICATION DATA:
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
              CLASSIFICATION:
                                          APPLICATION NUMBER:
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                            CITY:
                                                                                                                                                                                                                                          ADDRESSEE:
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77; Conservative
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                                                                                                                                                                                                                       E: Eli Lilly and Company
Lilly Corporate Center
                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                  Skatrud, Paul L.
                                                                                                                                                                                                                                                                                                                                    Peery, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359
                                                                                                                                                                                                                                                                                                  MULTIPLE DRUG RESISTANCE GENE
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                                              US/08/395,246C
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Version

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APPLICANT: Lynn boucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                 183 RLIGNYSLGGISTGERRRYSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRN 242
                                                                                                                                                                                                                                                                                                                                                              114 VELRRSIGYVIQQIGLMPHWTIREN----IVLVPKLLKWSKEKKDEKAKELIKLVDLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 KRAVDNISLDIQSGEFIAFIGTSGSGKTTAL-RMINRMIEATD--GQIMMNGKDVRNMNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 RQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRALRR---
                                                                                                                     GKTF1FVTHDMDEAIKLADKICIMSKGKVVQYDTPDNIL-----RYPAN------DFVR
                                                                                                                                                                           RIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYM 302
                                                                                                                                                                                                                                                                                                                                                                                                                          EQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSHVAD 182
DFI-----GQNRLIQDRPNMKSVESAMIKPV----TVKADDSLNDAVNIMRTRRVDTIFV
                                                            DLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLK-----NIERMKHLKTLPM
                                                                                                                                                                                                                                           EYLDRYP-AELSGGQQQRIGVVRALAAEQDIILMDEPFGALDPITRDTLQDLVKELQQKL
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25.2%; Pred. No. 1e-15;
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RESULT 14
US-09-134-001C-3641
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          GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                         Sequence 3641, Application US/09134001C Patent No. 6380370
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Plant, Thomas G. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                             688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 Q-----MSLVSQEPRLFAT-TIAENIRY-GIIGSRFEKESTYEIRKRVEAAARMANAHDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 EQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQ--KKVEAV--MAE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDQESQDGLYQKWQMMLAYALHVLPFSVVATMI-FSS--VCY-----WTLGLHPEVARF 499
                                                                                                                                                                                                                                                                                                                                                                             AGV--LVGSGFLR 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GYFSAALLA--PHLIGEFLTLVLLG--IVQNPNIVNSV------VALLSI 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%; Score 229; DB 1; 23.0%; Pred. No. 6.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35784
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RESULT 15
US-08-665-259-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/08665259 Patent No. 6028173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3641
LENGTH: 273
TELEFAX: (508) 872-541
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                 REFERENCE/DOCKET NUMBER: ICTELECOMMUNICATION INFORMATION:
                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Dugan, Deborah A
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local s. 62;
                                                                                                NAME: Dugan, Deborah A. REGISTRATION NUMBER: 37,315
                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                    TELEPHONE:
                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 ERLNISHLI-----NKNIAELSGGQQQRVLIARALISDPSVLVLDEPTNGIDAKHVSKFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 AELSISHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 -IYGHPIQFVD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 IFCGTPAEMLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 QDCFSYVLQ-----SDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 SLKISYVSQKASAFNAGFPASVKEVVLSGLTKTKKL-----FQRFNKNDYQ-KVTKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 KHYLENINIKINQGEFLAIVGPNGAGKSTLLKVI---LGLLPIQKGEIIVDGKPFKGNKS
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Klinger, Katherine W.
VENTION: NOVEL HUMAN CHROMOSOME 16 GENES.
                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dackowski, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burn, Timothy C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                    (508)
                                               872-8400
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                                                                                                                                                                                     US/08/665, 259
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                                                                                   IG5-9.1
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139

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TYPE: amino acid

TYPE: protocory: unknown

MOLECULE TYPE: protein

US-08-665-259-27

Query Match
Best Local Similarity 32.1%; pred. No. 7:3e-14;
Matches 69; Conservative 37; Mismatches 91; Indels 18; Gaps 8;

Oy 79 GQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYNGRALRRE--QFQDCFSYVLQSD 136

Ind GECFGLLGYNGAGKTSTFKMLTDDESTTG---GEAFVNGHSVLKDLLQVQGSLGYCPQFD 1160

Oy 137 TLLSSLTVRETLH-YTALLAIRRGNPGSFQKK VEAVMAELSLSHVADRLIGNYSLGGIS 194

Db 1161 VPVDELTAREHLQLYTRLRCI----PWKDEAQVVKWALEKLELTKYADRLFGYV-----S 1211

Oy 195 TGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRS 254

Db 1212 GGNKRKLSTAIALIGYPAFIFLDEPTTGMDPKARRFLWNLILDLIKTGRSVVLTSHS-ME 1270

OY 255 ELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGY 289

Db 1271 ECEALCTRLAIMVNGRLHCLGSIQHLKNRFGD-GY 1304

Search completed: June 11, 2003, 09:14:17
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OM protein

protein search, using sw model

456.5 454.5

T30567

hypothetical prote ABC transporter-li hypothetical

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GenCore version Copyright (c) 1993 - 2003

Compugen Ltd.

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Result
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Maximum Match
Listing first
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C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1;
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A:Molecule type: DNA
A:Residues: 1-725 <MON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 3
A; Note: T26I12.10
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
C;Accession: T47652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: cultivar Columbia; BAC clone T26I12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL132954
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                                                                                                                                                                                                                                                                                                                   182;
                                                                                                                                                                                                                                                                                                                                                                                                                     68 PVPYVLNENNLQYDVTLRRR----FGFSRQNGVKTLLDDVSGEASDGDILAVLGASGAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 PEPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSSGSGK
                                  SPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRV
                                                                                                                                                         SVFNGSPASLPGFFSDFGRPIPEKENISEFALDLV-----RELEGSNEGTKALVDFN
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NPSLFETF-ILAKRYMKNWIRMPELVGTRIATVMVTGC-LLATVYWKLDHTPRGA-QERL
                                                                                                                                                                                              LIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETS-------
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29.4%; Pred. No. 1e
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Gaps

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210 182 151 123 92

A; map position: sk C; Superfamily: ATP-dependent permease ADP1; ATP-bind C; Keywords: ATP; glycoprotein; nucleotide binding; P C; Keywords: Signal sequence #status predicted <si< th=""><th>Qy 65 TRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRA 119 :: : : : </th></si<>	Qy 65 TRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRA 119 :: : : :
tents: etics: e: SGD ss-refe	Query Match 18.9%; Score 627; DB 2; Length 1294; Best Local Similarity 31.7%; Pred. No. 1.1e-38; Matches 181; Conservative 106; Mismatches 228; Indels 56; Gaps 19;
m 10 **	F;1042-1058/Domain: transmembrane #status predicted <tm5> F;1015-1141/Domain: transmembrane #status predicted <tm5> F;117-1193/Domain: transmembrane #status predicted <tm6> F;117-1193/Domain: transmembrane #status predicted <tm7> F;1269-1285/Domain: transmembrane #status predicted <tm8></tm8></tm7></tm6></tm5></tm5>
nce number: S40914; MOID:92160395; PMID:178 ion: S40914 : not compared with conceptual translation le type: DNA es: 1-1049 <pur></pur>	F;469-485/Domain: transmembrane #status predicted <tm2> F;496-512/Domain: transmembrane #status predicted <tm3> F;606-622/Domain: transmembrane #status predicted <tm4> F;710-916/Domain: ATP-binding cassette homology <abc2></abc2></tm4></tm3></tm2>
:x59720; NID:g1907: .; Goffeau, A. the YCR105 gene loo	C; Superiamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology C; Keywords: ATP; nucleotide binding; P-loop; transmembrane protein F; 45-263/Domain: ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology F; 45-263/Domain: nucleotide-binding motif A (P-loop) F; 376-392/Domain: transmembrane #status predicted ATP-binding cassette homology F; 376-392/Domain: transmembrane #status predicted ATP-binding cassette homology F; 376-392/Domain: transmembrane #status predicted ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology F; 376-392/Domain: transmembrane #status predicted ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology ATP-binding cassette homology
Accession: S19421 Molecule type: DN Residues: 1-1049	s: SGD:S0005435 5L
<pre>C;Accession: S19421; S40914 R;Goffeau, A.; Purnelle, B.; Skala, J. submitted to the Protein Sequence Database, March 19 A;Reference number: S19420</pre>	A;Note: this was assumed to be the complete sequence of protein YOL075c C;Genetics:
X S I	A; MCJecule type: DNA A; MCJecule type: DNA A; Residues: 200-1294 <alf> A; Cross-references: EMBL: 274817 A; Cross-references: EMBL: 274817</alf>
RESULT 3 \$19421	
Qy 578 NEFYG-LNFTCGSSNVSVTTNPMCAFTQG 605	A;MCLECULE type: DNA A;Residues: 1-179,'TMTGVFLVVKRED' <alw> A;Cross-references: EMBL:Z74816</alw>
Qy 519 VLLGIVQNPN-IVNSVVALLSIAGVLVGSGFLRNIQE	Resi Cros Note
Qy 462 QMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARI	Alexan bmitte Refere Access
Qy 402 FEVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAV : : : : : : : : :	mes cha: -19: 776:
Qy 357 KTKDSPGVFSKLGVLLRRVTRNLV	RESULT 2 S77690 probable membrane protein YOL075c - yeast (Saccharomyces cerevisiae)
Qy 297 PFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSA :: : :: : : : Db 945 VADFFLDLISVNTQNEQNEISSRARVEKILSAWK	Oy 600 CAFTOGIQFIEKTCPGATS 618
Oy 239 AR-RNRIVVLTIHQPRSELFQLFDKIAILS-FGELIF	OY 540 AGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPM 599
Qy 179 HVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVML : : : : : : Db	OY 481 IPSSVCYWTIGLHPEVARFGYFSAALLAPHLIGEFUTLVLIGIVQNPNIVNS-VVALLSI 539 : ::: :
Qy 120 LRREQFQDCFSYVLQSDT-LLSSLTVRETLHYTALLA : :: :: : Db 765 VSELMFKNYCSYVSQDDDHLLAALTVKETLKYAAALR	QY 421 GLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATM 480
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NG 1250
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|: ::: |: | :|:
NVKRQETTTRRSEDSLMARIAQIPGLGVIFA 1053
                    2G 605
                                      MSL----GMSRVLKGFNYLNPVGYTSMIIIN 1223
                                                       SFLRNIQEMPIPFKIISYFTFQKYCSEILVV 577
                                                                                                                                                                                                   FVGMLGNLACYPTERDYFYEEYNDNVYGIA 1110
                                                                                                                                 PYTGMLNAVNLFPVLRAVSDQESQDGLYQKW 461
                                                                                                                                                                                                                                                                                 LODPKVMLFDEPTTGLDCMTANQIVVLLVEL 238
                                                                                                                                                                                                                                                                                                                          LHYTALLAIRRGNPGSFQKKVEAVMAELSLS 178
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16; PIDN:CAA42328.1; PID:g1907154; GSPDB: ted on the chromosome III from Saccharom MID:1789009 March 1992 r-1992 #text_change 19-Jan-2001 it (Saccharomyces cerevisiae)
YCR105

MID: 1626432 segment distal of SUF2 on the right arm .

ATP-binding cassette homology inding; P-loop; transmembrane protein cted <SIG>

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ABC transporter-like protein - Arabidopsis thaliana N;Alternate names: protein T15C9.80 C;Species: Arabidopsis thaliana (mouse-ear cress)
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50,114,165,221/Binding site: carbohydrate (Asn) (covalent) #status predicted
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1; Mismatches 223;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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A; Note: T15C9.80
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R; Lin, X. M.; Koo,

, X.; Kaul,

aul, S.; Moffat,

Rounsley, S.D.; Shea, T.P.; Bo K.S.; Cronin, L.A.; Shen, M.;

Benito, M.I.; Town, C.D.; Fujii, C.; VanAken, S.E.; Umayam, L.; Tallo

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C;Date: 20-Apr-2000 *sequ
C;Accession: T47648
R;Mewes, H.W.; Rudd, S.;
submitted to the Protein
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A; Residues: 1-720 <MEW>
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A; Accession: T47648
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                                                                              EFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKT
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-SDPTECFVRGVQLFDNS
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ced. No. 4.6e-38;
Mismatches 254
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ABC transporter-like protein - Arabidopsis thaliana
N; Alternate names: protein T15C9:110
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #te
C; Accession: T47650
R; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A; Reference number: 224470
A; Accession: T47650
A; Status: preliminary
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T47650
        A; Molecule type: DNA
A; Residues: 1-708 <MEW>
A; Cross-references: EMB
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A; Residues: 1-725 <STO>
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Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84423
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       Cross-references: EMBL:AL132970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRWAFQGLCINEFSGLKF
                                                                                                                                                                                                                                                                                  QKYCSEILVVNEFYGLNF
                                                                                                                                                                                                                                                                                                                                APHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTF
                                                                                                                                                                                                                                                                                                                                                                                                                       SA-----VIFGSVFWRMGKSQTSIQDRMGLLQVAAINTAMAALTKTVGVFPKERA
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                                                                                                                                                                                                                                                                                                          VESFAASAMGLTVGAMVPSTEAAMAVGPSLMTVFIVFG-GYYVNADNTPIIFRWIPRASL
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Pred. No. 8.6e-38;
L1; Mismatches 244;
                                                                                                                                  #text_change
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 A; Title: DNA sequence of the A; Reference number: S07263; M
                             R; O'Hare, K.; Murphy, C.; Le
J. Mol. Biol. 180, 437-455,
                                         A; Cross-references: EMBL: X51749; R; O'Hare, K.; Murphy, C.; Levis,
                                                                      A; Molecule type: mRNA
A; Residues: 1-687 < PEP>
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A; Note: T15C9.110
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27.5%;
e white locus of MUID:85134865;
                               1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Drosophila
5; PMID:6084717
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white protein - fruit fly (Drosophila melanogaster) (;Species: Drosophila melanogaster C;Date: 31-Dec-1990 *sequence_revision 17-Feb-1995 *text_chance_revision: $08635; $07263; $10240 R;Pepling, M.; Mount, S.M. Nucleic Acids Res. 18, 1633, 1990 A;Title: Sequence of a cDNA from the Drosophila melanogaster A;Reference number: $08635; MUID:90221897; PMID:2109311 A;Accession: $08635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVL 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPP-----LAETFILAKRYIKNWIRTPELIGMRIGTVMVTGLLLATVYWRL-DNTP 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSN 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARIIGLLDRLIILSHGKSVFNGSPVSLPSFFSSFGRPIPEKENITEFALDVIRELEGSSE
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NID:g8825; PIDN:CAA36038.1; PID:g8826 R.; Rubin, G.M.
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Pred. No. 1.3e-37;
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A;Introns: 24/3; 116/1; 334/2; 439/3; 483/3
A;Introns: 24/3; 116/1; 334/2; 439/3; 483/3
C;Superfamily: fruit fly white protein; ATP-binding cassette homology C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane F;113-317/Domain: ATP-binding cassette homology cABC>
F;130-137/Region: nucleotide-binding motif A (P-loop)
F;261-265/Region: nucleotide-binding motif B
F;67,93,472,554,651/Binding site: carbohydrate (Asn) (covalent) #status
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A;Residues: 1-24, 'LIFEIPYHCRVTAD', 30-687 <OHA2>
A;Cross-references: EMBL:X02974; NID:g10873; PIDN:CAA26716.1; PID:g10874
A;Experimental source: strain Canton S
C;Genetics:
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A;Residues: 1-24,'LIFEIPYHCRVTAD',30-334,'ITLHLNSYPAWVPSVLPTTIRRTFTYRCWPLCPDGRSSPVIGSPRY
A;Cross-references: EMBL:X02974
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                                                                 FIP----ALVILGIVVFKIRDHLISR
                                                                                                                           LVVNEFYGL---NFTCGSSNVSVTTNPMCAFTQGIQFIEKTCP--GATSRFTMNFLILYS 629
                                                                                                                                                             TSFGYLISCASSSTSMALSVGPPVIIPFLLEGGFFLNSGSVPVYLKWLSYLSWFRYANEG
                                                                                                                                                                                                                                                     VLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIV 530
                                           DLPLDYVGLAIL-IVSFRVLAYLALR
                                                                                                      LLINQWADVEPGEISCTSSNT
                                                                                                                                                                                                  NSVVALLS IAG-----
                                                                                                                                                                                                                             ELPLFLTVPLVFTAIAYPMIGLRAGVLHF----
                                                                                                                                                                                                                                                                                  V---GVMNINGAIFLELTNWTFQNVFATINVFTSELPVFMREARSRLYRCDTYFLGKTIA 513
                                                                                                                                                                                                                                                                                                                VLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGR--LGRAGTFLGEVYVNGRALRRE
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Pred. No. 3.2e-37;
31; Mismatches 220;
                                                                                                                                                                                      ----VLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEI 574
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A; Residues: 1-590 <STO>
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B96573
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TSRETMNELILYSEIPALVILGIVVEKIR : ::: | |: || || : |
                                              VYWEFMHYLSLFKYPFECLMINEY --
                                                                        IPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPGA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly
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29.6%;
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, Rizco, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Recession: B96573

A;Cession: B96573

A;Cession: B96573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 MCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PVKAPIPGGREISYRLETKNLSYRIGGNTPKFSNLCGLLSEKEEKVILKDVSCDARSAEI
DGFLYFSLVIWIVLLMSNSFVACFSALVPNFIMGTSVISGL-MGSFFLFSGYFIAKDRIP
                                                                                                                                                                                                                                                        RNLVRNKLAVITRLLQNLIMGLFLLFFYLRVRSNVLKGAIQDRVGLLYQFYGATPYTGML
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                                                ARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMP 556
                                                                                                                                                NAVNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEV
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                                                                                                     EGLPIFLQDRRILMRETSRRAYRVLSYVLADTLIFIPFLLIISMLFATPVYWLVGLRREL
                                                                                                                                                                                                        KNIFRTKQLFTTRALQASIAGLILGSIYLNV-GNQKKEAKVLRTG-FFAFILTFLLSSTT 400
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Pred. No. 6.7e-37;
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reasy, T.H.;
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A:Genetics:
A:Gene: CESP:F02E11.1 A:Hap position: 2
A:Hap position: 2
A:Introns: 115/3; 158/3; 214/3; 330/3; 368/2; 448/3; 525/1 C;Superfamily: fruit fly white protein; ATP-binding cassette homology
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A; Residues: 1-658 <FAV>
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GLVALKIR 653
                                                                                                                                                                                                                                                                                                                                    NVLKG-AIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYA
                                                                    CDLI----NPLNATTTGY-----CPASDGPGILTRRGIDTPLYANVLILFMSFFVYRII
                                                                                                          SSNVSVTTNPMCAFTQGIQFIEKTCP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPSSTVFRMFHKVCFMATGKTVYHGAVDRLCPFFDKLGPDFRVPESYNPADFVMSEISI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGISIGEKKRLAFACEILTDPKILFCDEPTSGLDAFMASEVVRALLDLANKGKTIIVVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGISTGERRRYSIAAQLLQDRKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQQVDLFCGTLTVREQLTYTAHMRMKNATVQQKMERVENVLRDMNLTDCQNTLIGIPNRM
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                                                                                                                                                                                  IVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCG
                                                                                                                                                                                                                        LAELPQYTILPMIYGTIIYWMAGLVASVTSFLVFVFVCITLTWVAVSIAYVGACIFGDEG
                                                                                                                                                                                                                                                              LHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPN
                                                                                                                                                                                                                                                                                                                                                                              GDDEDDGESRYNSTFGTQFEILLKRSLRTTFRDPLLLRVRFAQILATAILVGIVNWRVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SPETEQEDVTRIEYLIHEYQNSDIGTQMLK-------KTRTAVDEFGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCG--YPCPEHSNPFDFYMDLTSVD
                                                                                                                                                                                                                                                                                                  --LKGPTIQNLEGVMYNCARDMTFLFYFPSVNVITSELPVFLREHKSNIYSVEAYFLAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSGVAEPGEVLALMGGSGAGKTTLMNILAHLDTNGVEYLGDVTVNGKKITKQKMRQMCAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214/3; 330/3; 368/2; 448/3; 525/1 white protein; ATP-binding cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.9%; Score 595.5; DB 27.1%; Pred. No. 1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                  -VLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255;
                                                                                                        -GATSRFTMNFLILYSFIPALVIL 637
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C;Superfamily: Arabidopsis thaliana probable ATP-binding
C;Keywords: ATP
F;110-310/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AC004218; NID:g3355463; PIDN:AAC27826.1; PID:g3355464
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallor euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AC004697; NID:g3402671; PIDN:AAC28975.1; PID:g340267 A;Experimental source: cultivar Columbia R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998 A;Description: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence. A;Reference number: 214168 A;Accession: T00545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ATP-binding cassette protein T16B24.1 - Arabidopsis thaliana N;Alternate names: protein F12L6.1 C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 02-Mar-2001 C:Accession: T02567; T00545; C84816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: C84816
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R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thallana chromosome II BAC T16B24 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-740 <STO>
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A; Residues: 1-362 < ROW>
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                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 PFVLSEDNLTYNVS--VRPKLDFRNLFPRRRTEDPEIAQTARPKTKTLLNNISGETRDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 PHSLGILHASYSVSHRVRPWWD-----ITSCRQQWTRQILKDVSLYVESGQ
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                                                                                                                                                                                                                                                                    RVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLLS 140
                                                                                                                                                                                                                        RVSIGIDITHDPILLFLDEPTSGLDSTSAFMVVKVLKRIAQSGSIVIMSIHQPSHRVLGL
                                                                                                                                                                                                                                                                                                                                        MLTVEETLMFAAEFRLPRSLPKSKKKLRVQALIDQLGIRNAAKTIIGDEGHRGISGGERR
                                                                                                                                                                                                                                                                                                                                                                         SLTVRETLHYTALLAIRRGNPGSFQK-KVEAVMAELSLSHVADRLIGNYSLGGISTGERR 199
GTRGLIEFNKKWQEMKKQSNRQPPLTPPSSPYPNLTLKEAIAASISRGKLVSGGESVAHG 414
                                                                                                             LDRLIFLSRGHTVYSGSPASLPRFFTEFGSPIPENENRTEFALDLI-----RELEGSAG
                                                                                                                                                                     FDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKERE----
                                                           ----IETSKRVQMIE-----
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27.5%; Pred. No. 2.4e-36;
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                                                        -----SAYKKSAICHKTLKNIERMK--
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A;Gene: white C;Superfamily: fruit fly white protein; ATP-binding cassette homology C;Superfamily: fruit fly white protein; ATP-binding cassette homology C;Reywords: ATP; nucleotide binding; P-loop F;61-253/Domain: ATP-binding cassette homology <ABC> F;78-85/Region: nucleotide-binding mottif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Accession: G02068
R:Croop, J.M.; Tiller, G.; Fletcher, J.A.; Lux, M.; submitted to the EMBL Data Library, August 1995
A:Reference number: H00769
A:Accession: G02068
A:Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-638 < CRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 02-Feb-2001
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              CHKTLKNIERMKHLKTLPMVPFKTKDSPGV---
                                                LRDLGLNCPTYHNPADFVMEVASGEYGDQNSRLVRAVREGMCDSDHKRDLGGDAEVNPFL
                                                                                                                                                                                                                               FQKKVEAVMAELSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGL
                                                                                       FNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRVQMIESAYKKSA--
                                                                                                                            DSASCFQVVSLMKGLAQGGRSIICTIHQPSAKLFELFDQLYVLSQGQCVYRGKVCNLVPY
                                                                                                                                                SYSVPE--GPWW-----RKKGYKTLLKGISGKFNSGELVAIMGPSGAGKSTLMNILAGY-
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                                                                                                                                                                                                                                                                                    -RETGMKGAVLINGLPRDLRCFRKVSCYIMQDDMLLPHLTVQEAMWVSAHLKLQEKDEGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               17.8%; Score 590.5; DB 2; 26.3%; Pred. No. 2.3e-36; tive 142; Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   734
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            --FSKLGVLLRRVTRNLVRNKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, F.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ABC transporter [imported] - Arabidopsis thaliana
()Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
C; Superfamily: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE005172; NID:g11136734; PIDN:AAG31315.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-646 <STO>
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183; Conserv
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                                                                                                                                                                                                                                                                                                                 14 GGVMVQGLPDMSDTQSKSVLAFPTITSQP---GLQMSMYPITLKEVVYKVK-IEQTSQCM
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                        QIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGY 289
                                                                             RVIAELGLNRCINSMIGGPLFRGISGGEKKRVSIGQEMLINPSLLLLDEPTSGLDSTTAH
                                                                                                   AVMAELSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLEDEPTTGLDCMTAN 229
                                                                                                                                                          ----QPFSGCIKRRTGFVAQDDVLYPHLTVWETLFFTALLRL----PSSLTRDEKAEHVD
                                                                                                                                                                                                                                                              QQW---TRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGR 118
  RIVTTIKRLASGGRTVVTTIHQPSSRIYHMFDKVVLLSEGSPIYYGAASSAVEYFSSLGF
                                                                                                                                                                              ALRREOFODCE----SYVLOSDTLLSSLTVRETLHYTALLAIRRGNPGSFQK-----KVE 169
                                                                                                                                                                                                                                       GSWKSKEKTILNGITGMVCPGEFLAMLGPSGSGKTTLLSALGGRLSK--TFSGKVMYNG- 126
                                                                                                                                                                                                                                                                                                                                                       GGSM--GLQVNRGSQS-SLEGAPATAPEPHSLGILHASYSVS-----HRVRPWWDITSCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTHLRITSHIGIGLLIGLLYLGIGNEAKK--VLSNSGFLFFSMLFLMFAALMPTVLTFPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISYVRYGFEGVILS-IYGLD----REDLHCDIDETCHF-QKSEAILRELDVENAKLYLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISY 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                17.7%; Score 589.5; DB 2; 29.9%; Pred. No. 2.8e-36; 7ative 112; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     646;
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Maiti, R
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298
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Mars

197 MQDDLLFPMLTVEETLMFSAEFRLPRSLSKKKKARVQALIDQLGLRSAAKTVIGD 188 YSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVL 188 YSLGGISTGERRRVSIGNDIIHD :: : : : : : : : :	Qy 21 SQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWMDITSCRQQWTRQILKDV 72 : : : : : : : : :	Len, M.; Venaken, S.E.; Umayam, L. J.A.; Salzberg, S.L.; Fraser, C.N ne 2 of the plant Arabidopsis thal PMID:10617197 189; PIDN:AAC98055.1; GSPDB:GN0013 e ATP-binding cassette protein F1 pe-36;	VNEFYGLAFT 586 :	ر ر س س م م م س ا
OY 149 HYTALLAIRRGNPGSFQKKVEAVMAELSLSHVADRLIGNYSTGEDILMGTLTVRETI 122 OY 149 HYTALLAIRRGNPGSFQKKVEAVMAELSLSHVADRLIGNYSTGETITVRETI 121 OY 151 1	y Match 17.5%; Score 583.5; DB 2; Length 687; Local Similarity 28.0%; Pred. No. 8.6e-36; hes 167; Conservative 117; Mismatches 239; Indels 73; Gaps 16; 33 PEPHSIGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSS 88	Ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408; 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: D96553 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-687 <sto> A;Cross-references: GB:AE005173; NID:g10092349; PIDN:AAG12758.1; GSPDB:GN00141 C;Genetics: A;Gene: F5D21.6 A;Map position: 1 C;Superffamily: Arabidopsis thaliana probable ATP-binding cassette protein F1216.1: A</sto>	14 letical prices: Arabission: DZ-Mar- ssion: DZ-Mar- logis, A. C.W.; Ch	Db 371RELEYSTEGTKPLVEFHKQWRAKQAPSYNNNNKRNTNVSSLKEAITASISRGK 423 Oy 353MVP-FKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLF 399 424 LVSGATNNNSSNLTPSFQTFANP-FWIEMIVIGKRAILNSRRQPELLGMRLGAVMVTGII 482 QY 400 LLFFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQ 459

QY 379 LVRNKLAVITRLLQNLIMGLELLEFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNA 438	QY 327 SAYKKSAICHKTLKNIERMKHLKTLDMVDFKTKDSPGVFSKLGVLLRRVTRN 378	QY 267 SEGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRVQMIE 326	Qy 207 LLQDFKVMLFDEFTTGLDCMTANQIVVLLVELARRNRIVVLTIHQFRSELFQLFDKIAIL 266 : :	Qy 153 LLAIRRGNPGSFQKKVEAVMAELSLSHVADRLIGNVSLGGISTGERRRVSIAAQ 206 :	QY 93 TTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTA 152 ::	QY 33 PEPHSLGILHASYSVSHRVRPWMDITSCRQQWTRQILKDVSLYVESGQIMCIIGSSGSGK 92	Query Match 17.4%; Score 578.5; DB 2; Length 646; Best Local Similarity 27.1%; Pred. No. 1.9e-35; Matches 171; Conservative 126; Mismatches 274; Indels 59; Gaps 14;	A;Gene: abcg4 A;Map position: 11q23.3 C;Keywords: macrophage	** ** ** ** *	A;Contents: Macrophages A;Accession: JC7777 A;Molecule type: mRNA	R;Engel, T.; Lorkowski, S.; Lueken, A.; Rust, S.; Schlueter, B.; Berger, G.; Cullen, P.; Biochem. Biophys. Res. Commun. 288, 483-488, 2001 A;Title: The human ABCG4 gene is regulated by oxysterols and retinoids in monocyte-deriv A;Reference number; JC7777	707777 ATP binding cassette transporter, subclass G4 - human C:Species: Homo sapiens (man) C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002 C:Accession: JC7777	523 LITGAGIIGIIMMTSGFFRLLPD				VNLFPVL-	358 TWEKQLETLTKRSEVNMCRD		QY 323QMIESAYKKSAICHKTLKNIERMKHLKTLDMVPFKTKDSP 362
													Search completed: June 11, 2003, 09:13:51 Job time : 25 secs	Db 612 EDAKLYMDELVLGIFFLALRILAYLVLRYR 641	616 ATSRFTMNELILYSFIPALVILGIVVFKIR 645	QY 559 FKIISYFTFQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPWCAFTQGIQFIEKTCPG 615	Db 503 FLLFSALATATALVAQSLGL-LIGAASNSLQVATFVGPVTAIPVLLFSGFFVSFKTIPTY 561	499	QY 439 VNLFPVLRAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVAR 498 1	385

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Result
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649 5
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1 MGDLSSLTPGGSMGLQVNRG......PALVILGIVVFKIRDHLISR 651
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Copyright (c) 1993 - 2003 Compugen Ltd.
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0 Q9ARU4
0 Q9L182
0 Q9F1892
1 Q9FXN0
0 Q9LJC3
0 Q9LJC3
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Q96TA8
Q96LD6
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                                                       Q8r543 mus musculu
Q96ta8 homo sapien
Q96ta8 homo sapien
Q96t691 dictyosteli
Q9r004 mus musculu
Q9m3d6 arabidopsis
Q8rv19 arabidopsis
Q8rv19 arabidopsis
Q9aru4 oryza sativ
Q91182 arabidopsis
Q9fnb5 arabidopsis
Q9fnb5 arabidopsis
 Q9m2v7
Q9zu35
Q9asr9
                                                                                                                                                                                                         Description
                                 Q8rxn0 arabidopsis
Q91jc3 arabidopsis
7 arabidopsis
5 arabidopsis
9 arabidopsis
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RESULT 1 Q8R543

Q8R543

PRELIMINARY;

PRT;

673 ₿

Q8R543; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequ 01-JUN-2002 (TrEMBLrel. 21, Last anno

Last sequence update)
Last annotation update)

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                                                                  EMBL; AF3
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                      Lu K., Zhou Y., Lee M.-H., Patel S.B.;

Molecular cloning, genomic structure and characterization mouse head-to-head tandem ABC transporters.";
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                STRAIN-129/SV;
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
      195;
                   Similarity
   Conservative
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                                                               FA08340445DF259C CRC64;
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                     Komatani H., Kotani H., Hara Y., Nakagawa R., Matsumoto M., Arakawa H., Nishimura S.;
*Identification of breast cancer resistant protein/mitoxantrone resistance/placenta-specific, ATP-binding cassette transporter a transporter of NB-506 and J-107088, topoisomerase I inhibitors windolocarbazole structure. *;
Cancer Res. 61:2027-2032(2001).
EMBL, AB051855, BAB46933.1;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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          InterPro;
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(TrEMBLrel. 19, Last sequence update)
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Best Local :
                                                                                                                                                                                                                                                                                  Q96LD6;
                                                                                                                                                                                                      01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
01-JUN-2002 (TremBLrel.
                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003580; Protachykinin.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
SMART; SM00203; TK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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  SEQUENCE FROM N.A
                                                NCBI_TaxID=9606;
                                                                                                                                                       ABCG2.
                                                                                                                                                                                ABC transporter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYAL-HVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLLMTICEVEMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERE-----IETSKR-----VQMIESAYKKSAICHKT-----LKNIERMKHLKTLPMVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                          LNATGNNPCNYA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSVTTNPMCAFTQGIQFIEKTCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VALLSIAGY -- LVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLM---MVAYSASSMALAIAAGQSVVSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TT----SFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFL--LFFVLRVRSNVLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEDFKATEIIEPSKODKPLIEKLAEIYVNSSFYKETKAELHOLSGGEKKKKITVFKEISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIINGDSTAVALNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PG-LNAILGPTGGGKSSLLDVLAARKDPSG-LSGDVLING-APRPANFKCNSGYVVQDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVEKEILSNINGIMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003880;
IPR003580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       655 AA; 72314 MW;
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                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                ABCG2
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Last annotation update)
                                                                                                                                                                                                                                                         Created)
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Pred. No. 2.
                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             PRT;
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591 537 533 480

594

421 414 369 356 309 312

RA DR RT DR DR DR DR DR DR DR

Best Loc Matches

110;

Gaps

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The Human ABC Transporter, ABCG2, Transports Hoech Requires an Intact Walker A Motif.", Submitted (JAN-2001) to the EMBL/GenBank/DDBJ datab EMBL, AV017168; AAG52982.1; ANO17168; AAG52982.1; InterPro; IPR003439; ABC_transportr InterPro; IPR003880; Ppantne_attach. Pfam; PF00005; ABC_transportr; 1.

Pfam; PF00005; ABC_transportr; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.

SEQUENCE 655 AA; 72288 MM; B3B5DC02C095C4A8 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                Q8T691 PRELIMINARY;
Q8T691;
O1-JUN-2002 (TrEMBLEE1. 2
O1-JUN-2002 (TREMBLEE1. 2
O1-JUN-2002 (TREMBLEE1. 2
ABC transporter AbcG1.
             Dictyostelium discoideum (Slime mold)
Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
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                                                                                                                                                             PRELIMINARY;
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ABCG2, Transports
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Last sequence update)
Last annotation updat
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Pred. No. 1.1e
37; Mismatches
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Best Local
                                            01-MAY-2000 (TrEMBLrel. 13, Creat
01-MAY-2000 (TrEMBLrel. 13, Last
01-JUN-2002 (TrEMBLrel. 21, Last
Breast cancer resistance protein
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
                                                                                                                 Q9R004;
                                                                                                                                 Q9R004
                                  ABCG2 OR BCRP1
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"Evolution of the ABC transporters of Dictyostel Submitted (FEB-2002) to the EMBL/GenBank/DDBJ da EMBL; AF482380; AAL91485.1; -
SEQUENCE 801 AA; 90052 MW; CCC4F0036CB195A3
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SEQUENCE FROM N.A.
STRAIN=AX4;
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                                                                                                                                                                                                                                                                                                                                                                                           VYDTLPFFLAKSFMDACIAVLLPMVTATIVYWMTNQRVDPFYSAAPFFRFVLM---LVLA
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                                                                                                                            PRELIMINARY;
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Pred. No. 8.3e-40;
Craniata;
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Q9M3D6;
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PROSITE; PS00012; PHOSPHOPANTETHEINE
SEQUENCE 657 AA; 73021 MH; 207B7
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InterPro; IPR003880; Ppantne_attach.
Pfam; PF00005; ABC_tran; 1.
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Cancer Res. 59:4237-4241(1999).
EMBL; AF140718; AAD54216.1; -.
MGD; MGI:1347061; Abcg2.
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Allen J.D., Brinkhuis R.P., Wijnholds J., Schinkel A.H.;
"The mouse Bcrpl/Mxr/Abcp gene: amplification and overexpression
cell lines selected for resistance to topotecan, mitoxantrone, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FVB; TISSUE-LIVER;
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NCBI_TaxID=10090;
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                                                                                                                                                          YCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPG 615
                                                                                                                                                                                                                           IGEFLTLVLLGIVQNPNIVNSVVALLSIAGV--LVGSGFLRNIQEMPIPFKIISYFTFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTQS-----KEREIETSKR------VQMIESAYKKSAICHKTLKNIERMKHLKTLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGLQVNRGSQSSLEGAPATAPEPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDV
                                                                                                                    YGFTALQYNEFLGQEFCPG---FNVTDNSTCVNSYAI-----CTG 612
                                                                                                                                                                                                  VAYTASSMALAIATGQSVVSVATLLMTIAFVFMMLFSGLLVNLRTIGPWLSWLQYFSIPR
                                                                                                                                                                                                                                                                               YISGYYRVSSYFFGKVMSDLLPMRFLPSVIFTCILYFMLGLKKTVDAFFIMMFTLI---M
                                                                                                                                                                                                                                                                                                                     SQDGLYQKWQMMLAYAL-HVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHL
                                                                                                                                                                                                                                                                                                                                                              ILGLIIGAIYFDLKYDA----AGMQNRAGVLF-FLTTNQCFSSVSAVELFVVEKKLFIHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVPFKTKDSPGVFSKLGV---
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                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodentia; Sciurognathi; Muridae;
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"Full Length cDNA of gene T26I12.10/AT3g55130 (GI:7019646).";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding.
725 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABC transporter-like protein (Putative T26I12.10 OR AT3G55130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000006; ABC_transportr;
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                      PS00211; ABC_TRANSPORTER; UNKNOWN_1.
          LIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETS------
                                                      PIVLFLDEPTSGLDSTNAFMVVQVLKRIAQSGSIVIMSIHQPSARIVELLDRLIILSRGK
                                                                                     PKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGE 270
                                                                                                                                 SEFRLPRSLSKSKKMERVEALIDQLGLRNAANTVIGDEGHRGVSGGERRRVSIGIDIIHD
                                                                                                                                                                                                              STLIDALAGRVAE-GSLRGSVTLNGEKVLQSRLLKVISAYVMQDDLLFPMLTVKETLMFA
                                                                                                                                                                                                                                                      TTLLDAMSGRLGRAGTFLGEVYVNG-RALRREQFQDCFSYVLQSDTLLSSLTVRETLHYT 151
                                                                                                                                                                                                                                                                                                                                     PEPHSLGILHASYSVSHRVRPWWDITSCRQQWTRQILKDVSLYVESGQIMCILGSSGSGK
                                                                                                                                                                                                                                                                                                PVPYVLNFNNLQYDVTLRRR-----FGFSRQNGVKTLLDDVSGEASDGDILAVLGASGAGK
                                                                                                                                                                                                                                                                                                                                                                               Conservative 124;
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                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 649.5;
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                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                             246;
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Best Local Similarity
Matches 173; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 691 AA; 77219 MW; CE473CC0B440D7E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 77.2 kDa protein.
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                            GGERKRYSIALEILTRPQILFLDEPTSGLDSASAFFYIQALRNIARDGRTYISSVHQPSS
                                                                             TGERRRYSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRS
                                                                                                                                                                     SSLTVRETLHYTALLAIRRGNPGSFQKK-----VEAVMAELSLSHVADRLIGNYSLGGIS 194
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                                                                                                                                      QIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.9%; Score 628; DB 10; 28.1%; Pred. No. 2.1e-37; Live 123; Mismatches 225
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                                                                                                                                                                                                                                                                      C STRAIN-CV. NIPPONBARE;

A Sasaki T., Matsumoto T., Yamamoto K.;

TO STRAIN-CV. Nipponbare(GA3) genomic DNA, chromosome 1, F

RT Clone:P0445D12.*;

RT clone:P0445D12.*;

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

DR EMBL; AD003046; BAB40032.1; -.

DR InterPro; IPR00353; AAA_ATPase.

DR InterPro; IPR003439; ABC_transportr.

DR Pfam; PF00005; ABC_tran; 1.

DR ProDom; PD000006; ABC_transportr; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER; 1.

RW ATP-binding; Transport.

SQ SEQUENCE 668 AA; 73368 MW; D187588C7580F3B2 CRC64;

SQ SEQUENCE 668 AA; 73368 MW; D187588C7580F3B2 CRC64;
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Best Local Sim
Matches 171;
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Q9ARU4;
Q9ARU4;
Q1-JUN-2001 (TrEMBLrel. 17, C
Q1-JUN-2001 (TrEMBLrel. 17, I
Q1-JUN-2002 (TrEMBLrel. 21, I
Putative ABC transporter.
P04445D12.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pos
Ehrhartoideae; Oryzeae; Oryza.
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HLSGELYINGRPISEGGYK--IAYVRQEDLEFSQLTVRET CTREETON IN
           -FLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRG-NPGSFQK
                                                                                                                       WDITSC-----RQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGT- 108
                                                                                           WARITCALKNKRGDVARFLLSNASGEAKSGRLLALMGPSGSGKTTLLNVLAGQLTASPSL
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                                                                                                                                                                                                                                          18.7%; Score 622; DB 10; 31.0%; Pred. No. 5.4e-37;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                     DNA Res. 7:217-221(2000).
EMBL; AP001313; BAB03081.1; -
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003880; Ppantne_attach.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-COLUMBIA; Kaneko T., Kato T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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                                                                              ProDom; PD000006; ABC_transportr; 1.
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                        Structural analysis
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                                       PS00012; PHOSPHOPANTETHEINE;
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Last annotation update)
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EMBL/GenBank/DDBJ databases
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RESULT 10
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   Matches
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Best Local Similarity
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ABC transporter-like protein.
ARC transporter-like protein.
Arabidopsis trhaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                      Q9FNB5;
                                                           "Structural analysis of Arabidopsis Sequence features of the regions of physically assigned P1 clones."; DNA Res. 4:291-300(1997).
EMBL; AB006704; BAB08684.1;
                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-COLUMBIA;
InterPro; IPR003593; AAA_ArPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
                                                                                                                                           Kotani H., Nakamura
Tabata S.;
                                                                                                                                                                          MEDLINE-98069011; PubMed-9405937;
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Best Local S
Matches 179
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01-MAY-1997 (TrEMBLrel. 0:
01-MAY-1997 (TrEMBLrel. 0:
01-JUN-2002 (TrEMBLrel. 2
EYE pigment TANSPORTER (E
          SEQUENCE FROM N.A.
STRAIN-ROCKEFELLER;
MEDLINE-97418473; PubMed-9272447;
Coates C.J., Schaub T.L., Besansk
                                                                                                                             Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Nematoce
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PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
ATP-binding.
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80300 MW; 6345CCF5877213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTVRETLHYTALLAIRRGNPGSFQK-----KVEAVMAELSLSHVADRLIGNYSLGGISTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFVLSFTDLTYSVKVRRKFTWRRSVSSDPGAPSEGIFSSK---TKTLLNGITGEARDGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHSLGILHASYSVSHRVRPWW-------DITSCRQQWTRQILKDVSLYVESGQI
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 126;
                                                                                                                                                                                                                                                                                                                                                                                    -GDPTKCFVRGVQIFDNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.6%;
28.7%;
                                                                                                                                                                                                03, Created)
03, Last sequence update)
21, Last annotation updat
(EYE pigment transporter).
              Besansky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 617; DB 10;
Pred. No. 1.4e-36;
26; Mismatches 233;
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6345CCF5877213A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     612
                                                                                                                                                                                                                                                                                                                                                                                 648
            N.J.,
                                                                                                                                                                                                      notation update)
transporter).
                                                                                                                                                                                                                                                                                               692
                                                                                                                                                                                                                                                                                           A
            Collins
                                                                                                                                  Nematocera;
            13]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
          James
                                                                                                                                  Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310
                                                                                                                                                                                                                                                                                                                                                                                                                                                  631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
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     RESULT 12
Q8RXN0
ID Q8RXN
AC Q8RXN
DT 01-JU
DT 01-JU
DT 01-JU
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Best Local
   Q8RXNO;
01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                          Q8RXN0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coates C., Schaub T.L., James A.A.;
Submitted (FEB-1998) to the EMBL/GenBa
EMBL; U88851; BAC04894.1; -
EMBL; AF051096; AAC05165.1; -
InterPro; IPR003439; ABC_transportr.
InterPro; IPR005284; Pigment_permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ROCKEFELLER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-20 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The white gene from the yellow fever Insect Mol. Biol. 6:291-299(1997). [2]
                                                                                                                                                                                                  628
                                                                                                                                                                661
                                                                                                                                                                                                                                   620
                                                                                                                                                                                                                                                                                                        560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169;
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                                                                                                                                                              DEGEDIACLCMLIVIERL
                                                                                                                                                                                              -YSFIPALVILGIVVFKI
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                                                                                                                                                                                                                                 EALLINQWSTVQEGDIACTRANV
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 2 (TrEMBLrel.
2 (TrEMBLrel.
2 (TrEMBLrel.
                                                                      PRELIMINARY;
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Created)
Last sequence update)
Last annotation updat
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Pfam; PF00005; ABC_tran; 1.
ProDom; PD00006; ABC_transportr; 1.
TIGREAMS; TIGR00955; 3a01204; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
SEQUENCE 692 AA; 77231 MW; DF2F00EEB4C176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 RQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYV---NGRALRR
                                   EILVVNEFYGL---NFTCGSSNVSVTTNPMCAFTQGIQFIEKTCP--GATSRFTMNFLIL
                                                                               VATSFGYLISCASSSISMALSVGPPVIIPFLIFGGFFLNSASVPSYFEYLSYFSWFRYAN
                                                                                                                                                                                                      LHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVONPN
                                                                                                                                                                                                                                                                                                                                      PMEGASRTGYRSTWWTQFYYVLWRSWLTVLKDPMLVKVRLLQTAMVATLIGSIYFGQRLD
                                                                                                                                                                                                                                                                                                                                                                             PFKTKDSPGV----FSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFL--LFFVLRVR
                                                                                                                                                                                                                                                                                                                                                                                                                       DRLIGNYS-LGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHLLKNYTGMAKSGELLAVMGSSGAGKTTLLNALSFR-SPPGVKIAPTSVRALNGIPVNA
                                                                                                                                                                     IAEVPLFLAVPFVFTSITYPMIGLKSGAT---YYLTALLIVVLVA-----
                                                                                                                                                                                                                                                                                            SNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSDQESQDGLYQKWQMMLAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGKTIILTIHQPSSELYCLFDKILLVAEGRVAFLGSPYQASEFFSQLGIPCPPNYNPADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQLRARCAYVQQDDLFIPALTTREHLVFHAMLRWGKDVPKSVKMNRVNEVLQELSLAKCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQ-KKVEAVMAELSLSHVA
                                                                                                                                                                                                                                                    ---GVMNINGALFLFLINMTFQNVFAVINVFSAELPVFLREKRSRLFRVDTYFLGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%; Score 615; DB 5; 27.3%; Pred. No. 1.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DF2F00EEB4C17641 CRC64;
                                                                                                                         -VLVGSGFLRNIQEMPIPFKIISYFTFQKYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mosquito,
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TCPSSGQIILETFNFKVE
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122 17;

228

408 400 348

update)

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RESULT 13
09LJC3
1D 09LJC
AC 09LJC
DT 01-0C
DT 01-0C
DT 01-0C
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Best Local S
Matches 170
Q9LJC3
Q9LJC3;
Q9LJC3;
Q1-QCT-2000
Q1-QCT-2000
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Arabidopsis Full Length cDNA Clones.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY080792; AAL87274.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative ABC transporter AT1G17840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGS
                                                                                                                                                          GLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGV-LVGSGFL 549
                                                                                                                                                                                VTFMSIGGFPSFVEDMKVFQRERLNGHYGVAAFVIANTLSATPFLIMITFISGTICYFMV
                                                                                                RLPNDIPKPFWRYPMSYISFHFWALQGQYQNDLRGLTF
                                                                                                                    RNIQEMPIPF -- KIISYFTFQKYCSEILVVNEFYGLNF
                                                                                                                                        GLHPGFTHYLFFVLCLYASVTVVESLMMAIASIV--PNFLMGIIIGAGIQGIFMLVSGFF
                                                                                                                                                                                                     LNAVNL--FPVL---RAVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTL
                                                                                                                                                                                                                                              RNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRVGLLYQFV-----GATPYTGM
                                                                                                                                                                                                                                                                  AIRLLVDYYHTSDYYYTAKAKVEEISQFKGTIL-----DSGG--SQASFLLQ--TYTLT
                                                                                                                                                                                                                                                                                      RVQMIESAYKKSAICHKTLKNIERMKHLKTLPMVPFKTKDSPGVFSKLGVLLRRVTRNLV
                                                                                                                                                                                                                                                                                                           DAYEFFAQAGFPCPALRNPSDHFLRCINSDFDKVRATLKGSMKLRFEASDDPLEKITTAE
                                                                                                                                                                                                                                                                                                                                EMIDFFNDCGYPCPEHSNPFDFYMDLTSVD-------TQSKEREIETSK
                                                                                                                                                                                                                                                                                                                                                   MLRSEKRALVERTIIEMGLQDCADTVIGNWHLRGISGGEKRRVSIALEILMRPRLLFLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                      AANAFLSGTVLLNGR--KTKLSFGTAAYVTQDDNLIGTLTVRETIWYSARVRL----PDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSARL-TWQDLTVMVTMGDGETQNVLEGLTGYAEPGSLTALMGPSGSGKSTMLDALASRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSHRVRPWWDIT----SCRQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRL
                                                                                                                                                                                                                          KRSFINMSR-----DEGYYWLRLLIYILVTVCIGTIYLNVGTSYSAILARGSCASFVFGF
   O (TrEMBLrel. 15, 0) (TrEMBLrel. 15, 0) (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703
                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 112; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α̈́,
                                                                                                                                                                                                                                                                                                                                                                                                        -VEAVMAELSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDE
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29.4%; Pred.
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  Created)
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Pred. No. 2e
                                             PRT;
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   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
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Best Local S
Matches 173
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Kaneko T., Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          594 AA;
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAC and BAC clones.";
DNA Res. 7:217-221(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis
Sequence features of
TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: BELONGS TO THE ABC EMBL; AP000604; BAB01452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20363099; PubMed=10907853;
TLVLLGIVQNPNIVNSVVALLSIAG-VLVGSGFLRNIQEMP-----IPFKIISYFTFQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEGAPATAPE-PHSLGILHASYSVSHRVRPWWDITSCRQQW----TRQILKDVSLYVESG
                                                              YYGVSVYILSNYISSFPFLVAISVITGTITYNLVKFRPGFSHYAFFCLNIFFSVSVIESL
                                                                                                                                                                                                                                                                                     PFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLRVRSNVLKG
                                                                                                                                                                                                                                                                                                                                    TLKGSQRIQETPATSDPLMNLATSVIKARLVEN-YKRSKYAKSAKSRIRELSNIEGLEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGERRRYSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCFSYVLQSDYLL 139
                                                                                                        LYQKWQMMLAYALHVLPESVVATMIFSSVCYWTLGLHPEVAREGYESAALLAPHLIGEEL
                                                                                                                                                 ----SVGTIFYDVGYS-YTSILARVSCGGFITGFMTFMSIGGFPSFLEEMKVFYKERLSG
                                                                                                                                                                                                  AIQDRVGLLYQFVGATPYTGMLNAVNL----
                                                                                                                                                                                                                                            IRKGSEATW-WKQLRTLTARSFINMCRDVGYYWTRIISYIVVSI---
                                                                                                                                                                                                                                                                                                                                                                                    EIETSKRVQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIMAIMGPSGSGKSTLLDSLAGRLARNVVMTGNLLLNGKKARLD--YGLVAYVTQEDVLL
                                                                                                                                                                                                                                                                                                                                                                                                                          EVFALFDDLFLLSSGESVYFGEAKSAVEFFAESGFPCPKKRNPSDHFLRCINSDFDTVTA
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) to the H
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EMBL/GenBank/DDBJ databases.
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Query Match
Best Local (
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Mewes H.W., Rudd S., I
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL132970; CAB82704.1;
InterPro; IPR003593; AAA_ATPase
InterPro; IPR003439; ABC_transportr.
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720 AA;
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SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
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01-0CT-2000 (TrEMBLrel. 15, L
01-JUN-2002 (TrEMBLrel. 21, L
ABC transporter-like protein.
T15C9 an
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1999)
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                                                                                                   GGTRGLVEFNKKWQEMKKQSNPQTLTPPASPNP--NLTLKEAISASISRGKLVSGGGGGS
                                                                                                                                                                                            SHRVLSLLDRLIFLSRGHTVFSGSPASLPSFFAGFGNPIPENENQTEFALDLIRELEGSA
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                         SVINHGGGTLAVPAFANP ---
                                                       -----TLPMVPFKTKDSPGVFSKLGVLLRRVTRNLVRNKLAVITRLLQNLIMGLFLL
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28.7%;
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ke K., Mayer
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Pred. No. 2.3e-36;
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             -FWIEIKTLTRRSILNSRRQPELLGMRLATVIVTG-FIL
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K.F.X., Quetier
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Q920U5
ID Q9
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STRAIN-CY. COLUMBIA;

MEDILINE-20083487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                ATP-binding; Transport
SEQUENCE 725 AA; 78
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                       PROSITE; PS00211; ABC_TRANSPORTER; 1.
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Nature 402:761-768(1999).
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LSLSPRLHLSGLLEVNGKPSSSKAYK--LAFVRQEDLFFSQLTVRETLSFAAELQLPEIS
                                                                                                                 LGRAGT - - FLGEVYVNGRALRREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRR-G
                                                                                        IRPVTIRWRNITCSLSDKSSKSVRFLLKNVSGEAKPGRLLAIMGPSGSGKTTLLNVLAGQ
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                                                                                                                                                                                                                                                                             78899 MW;
                                                                                                                                                                                                            18.4%; Score 610.5; 29.7%; Pred. No. 4.1
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	591 IRWAFQGLCINEFSGLKF 608	591	망
	QKYCSEILVVNEFYGLNF 585	568	Qy
590	VESFAASAMGLTVGAMVPSTEAAMAVGPSLMTVFIVFG-GYYVNADNTPIIFRWIPRASL 590	532	Ф
567	APHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISVFTF 567	508	Q
531	472 IVDRERSKGSYSLGPYLLSKTIAEIPIGAAFPLMFGAVLYPMARLNPTLSRFGKFCGIVT 531	472	8
507	VSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALL 507	448	Ş
471	SAVIFGSVFWRMGKSQTSIQDRMGLLQVAAINTAMAALTKTVGVFPKERA 471	422	망
447	TRLLONLIMGLELLEFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRA 447	388	Qy
421	YATPLSMKEETKNGMRPRRKAIVERTDGWWRQFFLLLKRAWMQASRDGPTNKVRARMSVA 421	362	Дb
387	TRI	336	Оy
361	KEPLTYFGNFGFLCPEHVNPAEFLADLISVDYSSSETVYSSQKRVHALVDAFSQRSSSVL 361	302	₽,
335	-EMLDFFNDCGYPCPEHSNPFDFYMDLTSVDTQSKEREIETSKRYQMIESAYKKSAIC	279	9
301	TTGLDAFQAEKVMETLQKLAQDGHTVICSIHQPRGSVYAKFDDIVLLTEGTLVYAG-PAG 301	243	DЬ
278	TTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPA- 278	220	Qy
242	183 SAEERDEYVNNLLLKLGLVSCADSCVGDAKVRGISGGEKKRLSLACELIASPSVIFADEP 242	183	₽
219	NPGSFQKKVEAVMAELSLSHVADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEP	160	Ş

Search completed: June 11, 2003, 09:13:23 Job time: 43 secs

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Perfect score:
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd
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TYPE: PRT
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203	385	1642	1594	2436	2436	2436	1280	1280	1280	1279	247	241	345	242	306	1511	1501	1564	545	646	646	646	604	627	646
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US-10-252-819-17	US-09-769-787-144	US-09-971-121-2	US-09-971-121-4	US-09-795-693-8	US-10-199-485-8	US-10-156-239-8	US-09-866-866A-4	US-09-866-866A-2	US-10-072-621-7	US-10-097-340-2	US-09-738-626-5108	US-09-815-242-11194	US-09-815-242-11068	US-09-769-787-83	US-09-738-626-4554	US-09-801-368-250	US-09-801-368-346	'US-09-801-368-244	US-10-083-357-1335	US-10-154-452-8	US-10-090-455-13	US-10-154-452-4	US-09-745-763-197	US-10-090-455-8	us-10-090-455-2
17,	144,	Sequence 2. Appli	4.	œ. ≀	Sequence 8, Appli	.∞		e 2	•	Sequence 2, Appli	Sequence 5108, Ap	Sequence 11194, A	e 110	83, Ap	554		Sequence 346, App	244	Sequence 1335, Ap		13	Sequence 4, Appli	<u>ب</u>	80	Sequence 2, Appli

ALIGNMENTS

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; ORGANISM: Homo sapiens US-10-090-455-6
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Phiblication No. US20030027259A1
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/090,455
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND
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APPLICANT: Le Bihan;
                                                                                                                                                                                                            61 RQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRAL
                                                                                                                                                                                                                                                          RNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAENLDFFNDCGYPCPEHSNPFDF
                                                                              ADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR 240
                                                                                                                            RQQWTRQILKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTFLGEVYVNGRAL
                                                              ADRLIGNYSLGGISTGERRRVSIAAQLLQDPKVMLFDEPTTGLDCMTANQIVVLLVELAR
RNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEHSNPFDF
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100.0%; Pr
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Pred. No. 1.6e-289;
; Mismatches 0;
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; OTHER INFORMATION: human ABCG5 (hABCG5)
US-09-989-981A-6
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                                                                                                                                                                                                                                                                                 SEQ ID NO 6
LENGTH: 651
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hobbs, Helen H. APPLICANT: Shan, Bei
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 13 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/253,645 PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
FILE REFERENCE: 018781-0073200S
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                                             RREQFQDCFSYVLQSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSHV
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                                 RREQFODCFSYVLOSDTLLSSLTVRETLHYTALLAIRRGNPGSFQKKVEAVMAELSLSHV
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Pred. No. 1.6
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1.6e-289;
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LENGTH: 651
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: TULATİK Inc.

TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG):

TITLE OF INVENTION: and Methods of Use

FILE REFERENCE: 018781-006020US

CURRENT APPLICATION NUMBER: US/09/837,992

CURRENT FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: US 60/198,465

PRIOR FILING DATE: 2000-04-18

PRIOR FILING DATE: 2000-04-18

PRIOR FILING DATE: 2000-05-15
                                                                                                                                                             Query Match
Best Local Similarity
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APPLICANT: Schu
APPLICANT: Shan
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                                                                                                                      ; OTHER INFORMATION: mouse ABCG5 (mABCG5) US-09-989-981A-2
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US-09-989-981A-2
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Publication:No. US20030049730A1
FORMERAL INFORMATION:
                                                                                      Best Local :
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APPLICANT: Shan, Bei
APPLICANT: Barnes, Robert
APPLICANT: Tian, Hui
APPLICANT: Tularik Inc.
                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                        APPLICANT: Tian, Hui
APPLICANT: Tularik Inc.
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Method
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver.
                                                                                                                                                                 LENGTH: 652
TYPE: PRT
                                                                                                                                           ORGANISM: Mus musculus FEATURE:
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mes 523; Conserv
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Pred. No. 2.2
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Query Match
Best Local Similarity 80.2
Watches 523; Conservative
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                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                     APPLICANT: Tian,
APPLICANT: Schul
                                                                                                           LENGTH: 652
TYPE: PRT
                                                                                       ORGANISM: Mus musculus FEATURE:
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                     82.5%; Score 2744.5;
80.2%; Pred. No. 2.26
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; OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG); OTHER INFORMATION: amino acid sequence US-09-837-992-1
                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Pa+----
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                                                                                                                                                                                                                                                                 APPLICANT: Shan, Bei
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG):
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT FILING DATE: 2001-04-18
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Mismatches

Indels

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Gaps

Length 652;

.2e-237 DB 10;

Length 672; Indels

84;

Gaps

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APPLICANT: Tularik Inc.

APPLICANT: Board of Regents, The University of Texas System

TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use

FILE REFERENCE: 0.18781-007320US

CURRENT APPLICATION NUMBER: US/09/989,981A

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/252,235

PRIOR APPLICATION NUMBER: US 60/252,235

PRIOR ETLING DATE: 2000-11-20

PRIOR PRICATION NUMBER: US 60/253,645

PRIOR PRICATION NUMBER: US 60/253,645

PRIOR EPLING DATE: 2000-11-28

NUMBER OF EEG ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

IEDITAL 673
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hobbs, Held
APPLICANT: Shan, Bei
APPLICANT: Barnes, R
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                  ORGANISM: Mus musculus
   OTHER INFORMATION: mouse ABCG8 (mABCG8)
                        FEATURE:
                                                                           LENGTH: 672
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; ORGANISM: Homo sapiens
US-10-090-455-7
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                              NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 673
TYPE: PRT
                                                                                                                                                                                                                               Sequence 7, Application US/10090455 Publication No. US20030027259A1 GENERAL INFORMATION:
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Best Local 9
                                                                                                                                             APPLICANT: Chen, Hongyun
APPLICANT: Le Bihan, Stephane
TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND
FILE REFERENCE: 100103.406
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                                                                                                                        CURRENT APPLICATION NUMBER: US/10/090,455
CURRENT FILING DATE: 2002-03-01
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Local Similarity 29.1%;
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Pred. No. 9.4e-54;
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RESULT 8
US-09-989-981A-8
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                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
SEQ ID NO 8
                                                                                    APPLICANT: Tularix Inc.
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCC5 and ABCC8: Compositions and Method
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR PILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                     APPLICANT: Hobbs, Helen H.
APPLICANT: Shan, Bei
APPLICANT: Barnes, Robert
APPLICANT: Tian, Hui
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Best Local :
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                                                                                                                                                                                                                                                                     Sequence 1, Application US/09961086 Publication No. US20030036645A1 GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/961,086 CURRENT FILING DATE: 2001-09-21 PRIOR APPLICATION NUMBER: US 60/073,763 PRIOR FILING DATE: 1998-02-05 PRIOR APPLICATION NUMBER: PCT/US99/02577 PRIOR FILING DATE: 1999-02-05
                                                                                                                          TITLE OF INVENTION: BREAST CANCER RESISTANCE PROTEIN (BCRP) AND THE DNA TITLE OF INVENTION: WHICH ENCODES IT FILE REFERENCE: EP19376-019
                                                                                                                                                                                 APPLICANT: UNIVERSITY OF MARYLAND,
APPLICANT: ROSS, Douglas D.
APPLICANT: DOYLE, L. Austin
APPLICANT: ABBUZZO, Lynne
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ORGANISM: Homo sapiens
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RESULT 10

US-09-981-353-35

Sequence 35, Application US/09981353

Patent No. US20020160382A1

GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.

TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981,353

CURRENT FILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 194

SOFTMARE: PERL Program

SEQ ID NO 35
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US-09-961-086-1
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TYPE: PRT
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SOFTWARE: PatentIn Ver. 2.1
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RESULT 11
US-10-120-687-61
; Sequence 61, Application US/10120687
; Publication No. US20030082155A1
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; OTHER INFORMATION: Incyte ID No. US20020160382A1 5517972CD1
US-09-981-353-35
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                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Massachusetts General Hospital
TITLE OF INVENTION: Stem Cells of the Isl
TITLE OF INVENTION: Mellitus
FILE REFERENCE: 3284/1235B
                                                       CURRENT APPLICATION NUMBER: US/10/120,687 CURRENT FILING DATE: 2002-04-11 PRIOR APPLICATION NUMBER: US60/169082 PRIOR FILING DATE: 1999-12-06 PRIOR APPLICATION NUMBER: US 09/963,875 PRIOR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 182;
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              PRIOR APPLICATION NUMBER: US 60/215109 PRIOR FILING DATE: 2000-06-28
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FILING DATE:
APPLICATION |
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Pred. No. 2.7e-52;
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US-10-090-455-5
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US-10-120-687-61
                                                                                                                       Sequence 5, Application US/10090455
Publication No. US20030027259A1
GENERAL INFORMATION:
APPLICANT: Chen, Hongyun
APPLICANT: Le Bihan, Stephane
TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER
FILE REFERENCE: 100103.406
CURRENT APPLICATION NUMBER: US/10/090,455
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 655
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PRIOR APPLICATION NUMBER: US 09/731261
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.1
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US-09-866-866A-10
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                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09866866A Patent No. US20020102244A1
                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
                                                                                                                                                                                                                                                         APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying
FILE REFERENCE: 1340-1-021CIP2
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                                                                           PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1999-05-27
               PRIOR APPLICATION NUMBER: 60/086,988 PRIOR FILING DATE: 1998-05-28
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US-09-866-866A-27
Sequence 27, Application US/09866866A
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GENERAL INFORMATION:
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SEQ ID NO 10
         CURRENT APPLICATION NUMBER: US/09/866,866A CURRENT FILING DATE: 2001-08-30 PRIOR APPLICATION NUMBER: 09/584,586 PRIOR FILING DATE: 2000-05-31 PRIOR APPLICATION NUMBER: PCT/US99/11825 PRIOR FILING DATE: 1999-05-27 PRIOR APPLICATION NUMBER: 60/086,988
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                                                                                                                                     APPLICANT: Sorrentino, Brian
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-02101P2
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TYPE: PRT
ORGANISM: Homo sapien
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FILING DATE: 1998-05-28
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RESULT 15
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                                                                                                                                                                            Sequence 14, Application US/09866866A Patent No. US20020102244A1
                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version
SEQ ID NO 27
APPLICANT: Sorrentino, Brian
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying
FILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PG-LNAILGPTGGGKSSLLDVLAARKDPSG-LSGDVLING-APRPANFKCNSGYVVQDDV
                                                                                                                                                                                                                                                                                                   LNATGNNPCNYA----TCTG 610
                                                                                                                                                                                                                                                                                                                                          VSVTTNPMCAFTQGIQFIEKTCPG 615
                                                                                                                                                                                                                                                                                                                                                                            TLLMTICEVEMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEELGQNFCPG---
                                                                                                                                                                                                                                                                                                                                                                                                               VALLSIAGV--LVGSGFLRNIQEMPIPFKIISYFTFQKYCSEILVVNEFYGLNFTCGSSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEFLTLVLLGIVQNPNIVNSV 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKKITVFKEISY
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                                                                                                and/or Isolating
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473

480

414 369 356 309

421

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256 189 196 129 137 72

PRIOR APPLICATION NUMBER: PCT/US99/11825 PRIOR FILING DATE: 1999-05-27 PRIOR APPLICATION NUMBER: 60/086,988

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: PRIOR FILING DATE: 1998-05-28
: NUMBER OF SEQ ID NOS: 27
: SOFTMARE: PatentIn version 3.0
: SEQ ID NO 14
: LENGTH: 657
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-866-866A-14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 -----PGAQEKKGTSAFKEPVYVTSFCHQLRWIARRSFKNLLGNPQASVAQLIVTV 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 VQDDVVMGTLTVRENLQFSAALRL----PTTMKNHEKNERINTIIKELGLEKVADSKVGT 179
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YGFTALQYNEFLGQEFCPG---FNVTDNSTCVNSYAI-----CTG 612
                                                                                                                     YCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPG 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YISGYYRVSSYFFGKVMSDLLPMRFLPSVIFTCILYFMLGLKKTVDAFFIMMFTLI---M 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQDGLYQKWQMMLAYAL-HYLPFSVVATMIESSVCYWTLGLHPEVARFGYFSAALLAPHL 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LLRRVTRNLVRNKLAVITRLLQNL 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 657;
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Search completed: June 11, 2003, 09:14:46 Job time : 26 secs

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Result
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GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT:

APPLICANT:

Schultz, Joshua Shan, Bei Sequence 4, Application US/09837992 Patent No. US20020081687A1

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17 137 5.9 137 9 US-09-837-992-9 18 135.4 5.8 472 11 US-09-918-995-30637 Sequence 9, Appli 19 130 5.6 130 9 US-09-837-992-11 Sequence 13, Appl 129 5.5 129 9 US-09-837-992-11 Sequence 11, Appl 121 122 5.2 129 9 US-09-837-992-11 Sequence 11, Appl 221 114.2 4.9 2930 10 US-09-954-531-591 Sequence 5, Appl 122 114.2 4.9 2930 11 US-10-715-621-5 Sequence 5, Appl 123 114.2 4.9 3201 13 US-10-715-621-5 Sequence 5, Appl 125 113 4.8 113 9 US-09-837-992-18 Sequence 5, Appl 126 110.8 4.7 2687 13 US-10-72-621-5 Sequence 12, Appl 127 110.8 4.7 2687 13 US-10-90-455-12 Sequence 12, Appl 127 110.8 4.7 2687 13 US-10-90-455-12 Sequence 3, Appl 128 107.2 4.6 141 14 US-10-990-455-3 Sequence 12, Appl 139 107.2 4.6 3455 13 US-10-72-621-4 Sequence 7, Appl 139 107.2 4.6 3455 13 US-10-72-621-4 Sequence 7, Appl 130 107.2 4.6 3455 13 US-10-72-621-4 Sequence 1, Appl 131 107.2 4.6 3455 13 US-10-72-621-4 Sequence 1, Appl 132 103 4.4 103 9 US-09-897-992-10 Sequence 1, Appl 132 103 4.4 103 9 US-09-897-992-10 Sequence 2, Appl 132 103 4.4 103 9 US-09-897-992-10 Sequence 2, Appl 133 101.6 4.3 2648 11 US-09-981A-9 Sequence 2, Appl 138 98 4.2 2247 10 US-09-981-353-34 Sequence 2, Appl 138 98 4.2 2718 14 US-10-100-65-244 Sequence 2, Appl 139 98 4.2 2718 14 US-10-101-189-68 Sequence 3, Appl 140 90.4 3.9 2025 10 US-09-866-866A-26 Sequence 60, Appl 140 90.4 3.9 2025 10 US-09-866-866A-9 Sequence 60, Appl 140 90.4 3.9 2025 10 US-09-866-866A-26 Sequence 13, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 13, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 13, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 13, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 2022, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 2022, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 2022, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 2022, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 2022, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 2022, Appl 140 90.4 3.9 2025 10 US-09-866-866A-19 Sequence 2022, Appl 140 90.4 3.9 2025 10 US-	992-11 992-8 -531-591 -581-276 -621-5 992-18 992-18 992-10 -452-3 -455-1 -455-3 -621-4 -62	g g	103 6043 22470 2440 2574 2574 2718 2719 10330 2025 2025 2788 427		98 98 98 96 96 96 88 88 82 82 82 83	2 2 2 2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4
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137 5.9 137 9 US-09-8137-992-9 135.4 5.9 137 9 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-8137-992-13 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 114.2 4.9 2930 14 US-10-171-81-276 Sequence 114.2 4.9 2930 14 US-10-171-81-276 Sequence 113 4.8 131 US-10-072-621-5 Sequence 110.8 4.7 2687 13 US-10-194-452-3 Sequence 110.8 4.7 2687 14 US-10-090-455-12 Sequence 110.7.2 4.6 2687 13 US-10-194-452-7 Sequence 110.7.2 4.6 2687 13 US-10-090-455-3 Sequence 110.8 4.6 3455 13 US-10-090-455-1 110.7.2 4.6 3455 14 US-10-090-455-1 110.8 4.3 6043 11 US-09-981-992-10 Sequence 103 4.4 103 9 US-09-837-992-10 Sequence 104 4.3 6043 11 US-09-981-992-10 Sequence 105 4.3 6043 11 US-09-981-992-9	Sequence Sequence	q	103 6043 2247 2400 2418 2574	4.4.4	9 9 9 9	3333333 765432
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137 5.9 137 9 US-09-8137-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-8137-992-13 Sequence 120 5.5 129 9 US-09-837-992-11 Sequence 122 5.5 129 9 US-09-837-992-11 Sequence 122 5.2 122 9 US-09-837-992-11 Sequence 123 6.9 122 9 US-09-813-591 Sequence 124 6.9 2930 10 US-09-954-531-591 Sequence 125 127 9230 10 US-09-954-531-591 Sequence 127 108 113 9 US-09-817-922-18 Sequence 128 113 9 US-09-817-922-18 Sequence 129 110.8 4.7 2687 13 US-10-154-452-3 Sequence 120 120 120 120 120 120 120 120 120 120	Sequence Sequence	O O	103 6043 2247 2400	4.2	86	0 0 0 0 0 4 0 0
137 5.9 137 9 US-09-837-992-9 135.4 5.9 137 9 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 120 5.5 129 9 US-09-837-992-11 Sequence 122 5.2 122 9 US-09-837-992-11 Sequence 114.2 4.9 2930 14 US-10-171-581-276 Sequence 114.2 4.9 2930 14 US-10-072-621-5 Sequence 114.2 4.9 3201 13 US-10-072-621-5 Sequence 110.8 4.7 2687 13 US-10-154-452-3 Sequence 110.8 4.7 2687 14 US-10-090-455-1 Sequence 107.2 4.6 1941 14 US-10-090-455-1 Sequence 107.2 4.6 3455 13 US-10-072-621-4 Sequence 107.2 4.6 3455 14 US-10-090-455-1 Sequence 107.2 4.6 3455 14 US-10-090-455-1 Sequence 107.3 4.4 103 9 US-09-837-992-10 Sequence 108 4.2 2247 10 US-09-866-866A-26 Sequence 108 4.2 2247 10 US-09-866-866A-26 Sequence	Sequence Sequence 91 Sequence 76 Sequence Sequence Sequence Sequence Sequence 2 Sequence 2 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	0 0	103 6043 2247	4.2		333
137 5.9 137 9 US-09-837-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 114.2 4.9 2930 10 US-09-954-591 Sequence 114.2 4.9 2930 14 US-10-171-581-276 Sequence 114.2 4.9 3201 13 US-10-072-621-5 Sequence 110.8 4.7 2687 13 US-10-090-455-13 Sequence 110.8 4.7 2687 13 US-10-090-455-12 Sequence 107.2 4.6 1941 14 US-10-090-455-3 Sequence 107.2 4.6 3455 13 US-10-072-621-4 Sequence 107.2 4.6 3455 14 US-10-090-455-3 Sequence 108 4.4 3455 14 US-10-090-455-3 Sequence 109 4.4 103 9 US-09-837-992-10 Sequence 109 4.4 103 9 US-09-987-992-10 Sequence 100 4.3 6043 11 US-09-989-981A-9 Sequence	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	1 0	103 6043	,	98	33
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137 5.9 137 9 US-09-837-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 114.2 4.9 2930 10 US-09-954-531-591 Sequence 114.2 4.9 2930 11 US-10-171-581-276 Sequence 114.2 4.9 2930 12 US-10-172-621-58 Sequence 114.2 4.9 3201 13 US-10-072-621-58 Sequence 110.8 4.7 2687 13 US-10-154-452-3 Sequence 110.8 4.7 2687 14 US-10-090-455-12 Sequence 107.2 4.6 1941 14 US-10-090-455-3 Sequence	Sequence Sequence Sequence 91 Sequence 76 Sequence Sequence Sequence Sequence 2 Sequence 2 Sequence 2 Sequence		3455	4.6	107.2	30
137 5.9 137 9 US-09-837-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 130 5.5 129 9 US-09-837-992-11 Sequence 122 5.2 122 9 US-09-837-992-11 Sequence 114.2 4.9 2930 10 US-09-954-531-591 Sequence 114.2 4.9 2930 14 US-10-171-581-276 Sequence 114.2 4.9 2930 14 US-10-072-621-5 114.2 4.9 2930 13 US-10-072-621-5 110.8 4.7 2687 13 US-10-090-455-12 Sequence 110.8 4.7 2687 13 US-10-090-455-12 Sequence 110.8 4.7 2687 13 US-10-154-452-7 Sequence	Sequence Sequence 91 Sequence 76 Sequence Sequence Sequence Sequence Sequence		1941	4.6	107.2	29
137 5.9 137 9 US-09-918-995-9 135.4 472 11 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 129 5.2 122 9 US-09-837-992-11 Sequence 120 5.2 122 9 US-09-837-992-11 Sequence 114.2 4.9 2930 10 US-09-954-531-591 Sequence 114.2 4.9 2930 14 US-10-171-581-276 Sequence 114.2 4.9 3201 13 US-10-072-621-5 Sequence 110.8 4.7 2687 14 US-10-190-455-12 Sequence 110.8 4.7 2687 14 US-10-090-455-12 Sequence	Sequence Sequence 91 Sequence 76 Sequence Sequence Sequence Sequence		2687	4.6	107.6	28
137 5.9 137 9 US-09-837-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 130 5.6 130 9 US-09-837-992-11 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 129 5.2 122 9 US-09-837-992-1 Sequence 114.2 4.9 2930 10 US-09-954-531-591 Sequence 114.2 4.9 2930 14 US-10-171-581-276 Sequence 114.2 4.9 3201 13 US-10-072-621-5 Sequence 113 4.8 113 9 US-09-837-992-18 Sequence 110.8 4.7 2687 13 US-10-154-452-3 Sequence	Sequence Sequence Sequence Sequence Sequence Sequence Sequence		2687	4.7	110.8	27
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137 5.9 137 9 US-09-937-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 120 5.5 120 9 US-09-837-992-11 Sequence 122 5.2 122 9 US-09-837-992-8 124 5.2 122 9 US-09-837-992-8 125 5.2 120 9 US-09-837-992-8 126 5.9 130 US-09-954-531-591 Sequence 127 5.9 130 US-09-954-531-591 Sequence 128 5.9 137 902-954 130 10 US-09-954-531-591 Sequence 130 10 US-09-954-531-591 Sequence 130 10 US-09-954-531-591 Sequence 130 10 US-09-954-531-591 Sequence	Sequence Sequence 91 Sequence 76 Sequence Sequence	c	113	4.8	113	25
137 5.9 137 9 US-09-837-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 130 5.6 130 9 US-09-837-992-13 Sequence 129 5.5 129 9 US-09-837-992-11 Sequence 129 5.2 122 9 US-09-837-992-8 114.2 4.9 2930 14 US-10-171-81-276 Sequence 114.2 4.9 2930 14 US-10-171-81-276 Sequence	Sequence 91 Sequence 91 Sequence 76 Sequence		3201	4.9	114.2	24
137 5.9 137 9 US-09-837-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 9 130 5.6 130 9 US-09-837-992-13 Sequence 1 129 5.5 129 9 US-09-837-992-11 Sequence 1 122 5.2 122 9 US-09-837-992-8 Sequence 8 114.2 4.9 2930 10 US-09-954-531-591 Sequence	Sequence 11. Sequence 8, 91 Sequence 5		2930	4.9	114.2	23
137 5.9 137 9 US-09-837-992-9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 9 130 5.6 130 9 US-09-837-992-13 Sequence 1 129 5.5 129 9 US-09-837-992-11 Sequence 1 122 5.2 122 9 US-09-837-992-8 Sequence 8	Sequence 11, Sequence 8,		2930	4.9	114.2	22
137 5.9 137 9 US-09-837-992-9 Sequence 9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 1 130 5.6 130 9 US-09-837-992-13 Sequence 1 129 5.5 129 9 US-09-837-992-11 Sequence 1	Sequence 11,		122	5.2	122	12
137 5.9 137 9 US-09-837-992-9 Sequence 9 135.4 5.8 472 11 US-09-918-995-30637 Sequence 1 130 5.6 130 9 US-09-837-992-13 Sequence 1			129		129	20
137 5.9 137 9 US-09-837-992-9 Sequence 9 135.4 5.8 472 11 US-09-918-995-30637 Sequence	Sequence 1		130	5	130	. 19
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                                                                          Query Match
Best Local Similarity
Matches 2340; Conserv
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SEQ ID NO 4
LENGTH: 2340
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/204,234 PRIOR FILING DATE: 2000-05-15 NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/837,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tularik Inc.
TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG): Compositions
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 018781-006020US
                                                                                                                                               FEATURE: OTHER INFORMATION: human sitosterolemia gene (SSG)
NAME/RBY: CDS
LOCATION: (107)..(2062)
OTHER INFORMATION: human sitosterolemia susceptibility gene (SSG)
OTHER INFORMATION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                           TYPE: DNA
Conservative
                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-04-
                                                                                          Score 2340;
Pred. No. 0;
                                                                        Mismatches
                                                                                                         DB
                                                                        0;
                                                                      Indels
                                                                                                         Length 2340;
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64 B 64

Db 2221 TTGAATGCAATGGAAGTGGTTTATAGTCCCTTGCTCTTACAACTTGCAGGACATGTGGT 2280	рь	421 CGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGGCGCTGCGCCGGGAGCAGTT 480
Qy 2281 TATTIGGAAATTGTGACTGAGCGGACCCAAGAATGTAAATATATACATAAACCTATGGG 2340	Qy Db	481 CCAGGACTGCTTCTCCTACGTCCTGCAGAGCGACACCCTGCTGAGCAGCCTCACCGTGCG
RESULT 2	Qy Db	.541 CGAGACGCTGCACTACACCGCGCGCTGCTGGCCATCCGCCGCGGCAATCCCCGGCTCCTTCCA
ence 5, A	Qy	
; GENERAL INFORMATION: ; APPLICANT: Hobbs, Helen H.	дь	601 GAAGAAGGTGGAGGCCGTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGAT
Shan, Bei Barnes, Rob	Qy	661 TGGCAACTACAGCTTGGGGGGCATTTCCACGGGTGAGCGGGGCGCGGGTCTCCCATCGC
Tian, Hui Tularik Inc.	Db	661 TGCCAACTACAGCTTGGGGGGCATTTCCACGGGTGAGCGGCGCCGGGTCTCCATCGCAGC
APPLICANT: Board of Regents, The University of Texas System TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use	Qy	721 CCAGCTGCTCCAGGATCCTAAGGTCATGCTGTTTGATGAGCCAACCACAGGCCTGGACTG
	Db	721 CCAGCTGCTCCAGGATCCTAAGGTCATGCTGTTTGATGAGCCAACCACAGGCCTGGACTG
PRIOR APPLICATION UMBER: US 60/252,235	Qy	781 CATGACTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTGGCTCGCAGGAACCGAATTGT
PRIOR APPLICATION COMBER: US 60/253,645	Дb	781 CATGACTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTGGCTCGCAGGAACCGAATTGT
NUMBER OF SEQ ID NOS: 13	Qy	841 GGTTCTCACCATTCAGCCCCGTTCTGAGCTTTTTCAGCTCTTTGACAAAATTGCCAT
SEQ ID NO 5	Дb	841 GGTTCTCACCATTCACCAGCCCCGTTCTGAGCTTTTTCAGCTCTTTGACAAAATTGCCAT
てァ	Qy	
FEATURE: NAME/KEY: CDS	Ü	
LOCATION: OTHER INFO S-09-989-981	Db	961 TGACTGCGGTTACCCTTGTCCTGAACATTCAAACCCTTTTGACTTCTATATGGACCTGAC
Query Match 100.0%; Score 2340; DB 11; Length 2340; Best Local Similarity 100.0%; Pred. No. 0; Matches 2340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy Db ·	1021 GTCAGTGGATACCCAAAGCAAGGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGAT
1 GTCAGGTGGAGCAGGCAGGCAGGCAGTCTGCCACGGCCTCCCCAACTGAAGCCACTCTGGGGA 60	p Qy	1081 AGAATCTGCCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAAT
61 1	Qy i	141
Db 61 GGGTCCGGCCACAAAAATTTGCCCAGCTTTGCTGGTGACCATGGGTGACCTCTC 120	ДĎ	11111111111111111111111111111111111111
	Db Qy	1201 CTCTAAACTGGGTGTTCTCCTGAGGAGAGTGACAAGAACTTGGTGAGAAATAAGCTGGC
QY 181 GGAGGGGCTCCTGCCACCGCCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTA 240	Qy	1261 AGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTCTTTTCTTCGTTCT
Db 181 GGAGGGGCTCCTGCCACCGCCCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTA 240	מנו	
	D Qy	1321 GCGGGTCCGAAGCAATGTGCTAAAGGGTGCTATCCAGGACCGCGTAGGTCTCCTTTACCA
241	2	
QY 301 CAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCT 360	Db Q	1381 GTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAAACGCTGTGAATCTGTTTCCCGTGCT
	Qy	1441 GCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGAAGTGGCAGATGATGCT
Db 361 AGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCG 420	рф	
QY 421 CGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGCGCTGCGCCGGGAGCAGTT 480	D _b Qy	1501 GGCCTATGCACCTGCACGTCCTCCACCGTTGTTTGCCACCATGATTTTCAGCAGTGT

Gaps

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APPLICANT: Tularik Inc.
TITLE OF INVENTION: Sitosterolemia Susceptibility Ger
TITLE OF INVENTION: Sitosterolemia Susceptibility Ger
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 010791-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR FILING DATE: 2000-05-15
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APPLICANT: Tian, Hu
APPLICANT: Schultz
APPLICANT: Shan, B
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Patent No. US20020081687A1
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Schultz, Joshua
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NAME/KEY: CDS
LOCATION: (47)...(2005)
OTHER INFORMATION: mouse sitosterolemia susceptibility
OTHER INFORMATION: protein
US-09-837-992-2
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Best Local Similarity
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ORGANISM: Mus musculus
FEATURE:
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58.4%;

Score 1365.4; Pred. No. 0; Mismatches

DB 11; Length 1959;

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                                                 CTCATCTTATATGGGTTTATCCCAGCTCTGGTCATCCTAGGAATAGTGATTTTTAAAGT
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APPLICANT: Tularik Inc.

APPLICANT: Board of Regents, The University of Texas Systitle De Invertion: ABCG5 and ABCG8: Compositions and METILE REFERENCE: 018781-007320US

CURRENT APPLICATION NUMBER: US/09/989,981A

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/252,235

PRIOR APPLICATION NUMBER: US 60/253,645

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1959)
; OTHER INFORMATION: mouse ABCG5 (mABCG5)
US-09-989-981A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09989981A
Publication No. US20030049730A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hobbs, Helen H.
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Tian, Hui
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    GGATATITTTCTGCTGCTCCTTTGGCCCCCCACTTAATTGGTGAATTTCTAACTCTTGTG
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APPLICANT: Tularik Inc.

TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSI TITLE OF INVENTION: And Methods of Use FILE REFERENCE: 018781-006020US

CURRENT APPLICATION NUMBER: US/09/837,992

CURRENT FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: US 60/198,465

PRIOR FILING DATE: 2000-04-18

PRIOR FILING DATE: 2000-05-15

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 19

LENGTH: 472
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Matches 472
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Patent No. US20020081687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tian, Hui
APPLICANT: Schultz, Joshua
APPLICANT: Shan, Bei
APPLICANT: Tularik Inc.
                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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ATTCATTTATTCCAGCTCTTGTCATCCTAGGAATAGTTGTTTTCAAAATAAGGGATCATC
                                               TGTGCCTTCACTCAAGGAATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAGA
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US-09-837-992-7
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Best Local :
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SEQ ID NO 7
LENGTH: 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09837992
Patent No. US20020081687A1
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/204,234 PRIOR FILING DATE: 2000-05-15 NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG): Compositions TITLE OF INVENTION: and Methods of Use FILE REFERENCE: 018781-006020US
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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                      CAGCGTCAG 249
                                       GGAGGGGGCTCCTGCCACCGCCCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTA
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Schultz, Joshua
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; TYPE: DNA; ORGANISM: Homo sapiens; FEATURE: TYPE: TYPE AND SAPIENS; OTHER INFORMATION: exon 8 of hSSG US-09-837-992-14
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Patent No. US20020081687A1
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APPLICANT: TULATIK INC.

TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG):

TITLE OF INVENTION: and Methods of Use

FILE REFERENCE: 018791-006020US

CURRENT APPLICATION NUMBER: US/09/837,992

CURRENT FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: US 60/198,465

PRIOR FILING DATE: 2000-04-18

PRIOR APPLICATION NUMBER: US 60/204,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 214
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                                                                                                                                                         1131 TTGAAAGAATGAAACACCTGAAAACGTTACCAATGGTTCCTTTCAAAAACCAAAGATTCTC 1190
181 CTGGAGTTTTCTCTAAACTGGGTGTTCTCCTGAG 214
                                                                             121 TTGAAAGAATGAAACACCTGAAAACGTTACCAATGGTTCCTTTCAAAACCAAAGATTCTC
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                                        CTGGAGTTTTCTCTAAACTGGGTGTTCTCCTGAG 1224
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                   9.1%; Score 214; DB 9; 100.0%; Pred. No. 3.2e-54;
                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Length 214;
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RESULT 8
US-09-837-992-15
Sequence 15, Application US/09837992
Patent No. US20020081687A1
GENERAL INFORMATION:
APPLICANT: Schultz, Joshua
APPLICANT: Schultz, Joshua
APPLICANT: Tilarik Inc.
TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG):
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR APPLICATION NUMBER: US 60/204,234
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PRIOR APPLICATION NUMBER: US 60/204,234

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; LOCATION: (100)..(2121)
; OTHER INFORMATION: human ABCG8 (hABCG8)
US-09-989-981A-7
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US-09-989-981A-7
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                                                                                                                                                                                                   Query Match 8.7%;
Best Local Similarity 54.4%;
Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. SEQ ID NO 7
LENGTH: 2669
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tularik Inc.
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
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APPLICANT: Shan,
APPLICANT: Barnes
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                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo
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                                                                                      AGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGACGCCATGT
CTGGCCGAGGTCACGGCGGCAAGATCAAGTCAGGCCAGATCTGGATCAATGGGCAGCCCA 514
                               GGGTGCTATCCAGGACCGCGTAGGTCTCCTTTACCAGTTTGTGGGCGCCCACCCCGTACAC 1404
                                                                 AGATGCTGGCCATCATAGGGAGCTCAGGTTGTGGGAGAGCCTCCTTGCTAGATGTGATCA
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Pred. No. 2.8e-50;
0; Mismatches 359;
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                                  SEQ ID NO 3
LENGTH: 2019
TYPE: DNA
ORGANISM: Mus n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09989981A Publication No. US20030049730A1
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                       APPLICANT: Tularik Inc.
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
                                                                                                                          SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hobbs, Hel
APPLICANT: Shan, Bei
NAME/KEY: CDS
                  FEATURE:
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US-09-837-992-17

; Sequence 17, Application US/09837992

; Patent No. US20020081687A1
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: OTHER INFORMATION: mo
US-09-989-981A-3
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                                                       GENERAL INFORMATION:
APPLICANT: Tian, Hui
APPLICANT: Schultz, Joshua
APPLICANT: Shan, Bei
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430; Conserv
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; OTHER INFORMATION: exon 6 of hSSG US-09-837-992-12
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US~09-837-992-12
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                                                                                     SOFTWARE: PatentIn Ver.
SEQ ID NO 12
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tian, Hu
APPLICANT: Schultz
                                                                                                                                                                                                                                                                                                                                       Patent No. US20020081687A1
                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09837992
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
                                                                                                                                                                               TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG): TITLE OF INVENTION: and Methods of Use FILE REFERENCE: 018781-006020US CURRENT APPLICATION NUMBER: US/09/837,992 CURRENT FILING DATE: 2001-04-18
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                                                                                                                              PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR FILING DATE: 2000-05-15
                                                         LENGTH: 14
                                                                                                                NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                APPLICANT:
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TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG):
TITLE OF INVENTION: and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT FILING DATE: 2001-04-18
                               FEATURE:
                                           ORGANISM: Homo sapiens
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Shan, Bei
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Query Match Best Local Similarity

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Score 140; DB 9; ; Pred. No. 6.6e-32;

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RESULT 14
US-10-027-632-152156
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                                                     Sequence 152156, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SEQ ID NO 152155
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              CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 2000-07-12
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99.3%;
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Pred. No. 2.9e-31;
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; ORGANISM: Human US-10-027-632-152157
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SEQ ID NO 152157
       Best Local Similarity Matches 139; Conser
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SEQ ID NO 152156
LENGTH: 759
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                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/198,676
FILING DATE: 2000-04-20
APPLICATION NUMBER: US 60/193,483
FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/218,006 FILING DATE: 2000-07-12
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Search completed: July 27, 2003, 08:56:04 Job time : 501.926 secs	162 TCAGCAGTGTGTGCTACTGG 181	1551 TCAGCAGTGTGTGCTACTGG 1570	102 AGATGATGCTGGCCTATGCACTGCACGTCCTCCCCTTCAGCGTTGTTRCCACCATGATTT 161	1491 AGATGATGCTGGCCTATGCACTGCACGTCCTCCCCCTTCAGCGTTGTTGCCCACCATGATTT 1550	42 TTCCCGTGCTGCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGAAGTGGC 101	1431 TTCCCGTGCTGCGAGCTGTCAGCGACCAGGAGGAGTCAGGACGGCCTCTACCAGAAGTGGC 1490

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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SUMMARIES

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AAD22009 standard; DNA; 2340 BP

AAD22009;

12-FEB-2002 (first entry)

Human sitosterolaemia susceptibility gene (SSG).

Human; sitosterolaemia susceptibility gene; SSG; atherosclerosis; sterol-related disorder; hyperlipidaemia; hypercholesterolaemia; therapy; gall stone; coronary heart disease; cardiovascular disease; arthritis; xanthoma; haemolytic anaemia; transgenic animal; chromosome 2p21; ds.

FT ETH XXX Homo sapiens

CDS /*tag= a /product= "Human SSG protein" Location/Qualifiers

WO200179272-A2

PFXX 18-APR-2001; 2001WO-US12758 25-OCT-2001

18-APR-2000; 2000US-198465P. 15-MAY-2000; 2000US-204234P.

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CC The invention relates to an isolated Sitosterolaemia Susceptibility Gene CC (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) CC binding cassette (ABC) family cholesterol transporter. SSG is useful CC for identifying a compound useful in the treatment or prevention of a CC sterol-related disorder, including sitosterolaemia, hyperlipidaemia, CC hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or nutritional deficiencies. SSG is also useful for treating cholesterol-cC associated diseases or conditions including coronary heart disease and CC other cardiovascular diseases, and sitosterolaemia-associated condition including arthritis, xanthomas and chronic haemolytic anaemia. SSG cexpression cassette is useful in the production of transgenic non-human CC animals. SSG genes and their homologues are useful as tools for a number CC ardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The present sequence is human SSG DNA. Human SSG is located on chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local Similarity
Matches 2340; Conserv
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28-NOV-2000;
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             25-SEP-2001;
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                                                                                                     Human ABCG5
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                                                                                    cassette gene 5; sitosterolemia; cholesterol;
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                                                                             hypersterolemia;
                                                                             Alzheimer's disease;
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                                                                                                                                                                                                                                                                                                                                                                                           CC The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying CC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal. CC where an increase or decrease in ABCG5 biological activity in a control cell culture or in mammal. CC where an increase or decrease in ABCG5 biological activity on a control cell culture or mammal not CC contacted with the compound, identifies a compound that increases or CC contacted with the compound, identifies a compound that increases or CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC polypeptide in a cell culture or mammal is also compared with that of a CC second cell culture or mammal is also compared with that of a CC simulation of ABCG5 activity is useful for treating or preventing CC hypersterolemia, arteriosclerosis, heart disease and/or Alzhelmer's CC disease. The method of the invention is useful for increasing cholesterol CC acid sequence represents the CDNA sequence of human ABCC5 gene located XX on chromosome 2p21.
                                                                                                                                                                                                                                                                                                                                                 Matches 2339;
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel mammalian ATP-binding cassette gene 5 polypeptide, an nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
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                                                                                                                             GCGGGTCCGAAGCAATGTGCTAAAGGGTGCTATCCAGGACCGCGTAGGTCTCCTTTACCA
                                                                                                                                                                      AGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTTTCTTCGTTCT
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Best Local Similarity
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ACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCGCGCGGGGACCTTCCTGGGGGAG

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382 180

CCCTGGTGGGACATCACATCTTGCCGGCAGCAGTGGACCAGGCAGATCCTCAAAGATGTC

263 61 203

143 ATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCTGGAGGGGGCTCCTGCCACCCCC

Conservative

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82.1%; 100.0%;

Score 1920; Pred. No. 0; Mismatches

DВ 24; 0

Length 1920;

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ATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCTGGAGGGGGCTCCTGCCACCGCC

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The present invention relates to a new mammalian ATP-binding cassette C gene 5 (ABCG5) polypeptide. The invention is useful for identifying a C predisposition for developing sitosterolemia, arteriosclerosis or heart C disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell culture or mammal which have ABCG5 polypeptide with a compound and c measuring ABCG5 biological activity in the cell culture, or in mammal. C where an increase or decrease in ABCG5 biological activity compared to contacted with the compound, identifies a compound that increases or decreases ABCG5 activity respectively. The cell culture or mammal not c decreases ABCG5 activity respectively. The cell culture or mammal c c polypeptide or a wild type polypeptide. The C ABCG5 biological activity, or level of ABCG5 BRNA, or level of the c polypeptide in a cell culture or mammal is also compared with that of a c second cell culture or mammal comprising a wild type ABCG5 polypeptide. Simulation of ABCG5 activity is useful for treating or preventing c disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present nucleic carid sequence represents the human ABCG5 gene located on chromosome 2p21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel mammalian ATP-binding cassette gene 5 polypeptide, nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases
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/transl_except= (pos: 4..9, aa:
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Mouse; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
                                                                                             Mouse ABCG5
                                                                                                                                                  30-JUL-2002
                                                                                                                                                                                                     ABK51685
                                                                                                                                                                                                                                                             standard;
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CDNA

(first

entry)

CDNA;

2354 ΒP

W0200227016-A2

25-SEP-2001; 2001WO-US29859

25-SEP-2000; 2000US-235268P

PATEL S
DEAN M. Dean × HEALTH & HUMAN SERVICES

Novel mammalian ATP-binding cassette gene 5 polypeptide, an nucleic acid encoding the polypeptide, useful for treating sitosterolemia, arteriosclerosis and heart diseases

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying C a compound which alters ABCG5 activity level comprising contacting a cell CC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal, which have ABCG5 polypeptide with a compound and CC where an increase or decrease in ABCG5 biological activity compared to CC ABCG5 biological activity in a control cell culture or mammal not CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC ABCG5 biological activity respectively. The cell culture or mammal CC second cell culture or mammal is also compared with that of a Second cell culture or mammal comprising a wild type ABCG5 polypeptide. CC the invention of ABCG5 activity is useful for treating or preventing CC disease. The method of the invention is useful for increasing cholesterol activenting the present nucleic activenting energy and second cell culture or mammal comprisions. The present nucleic carid sequence represents the cDNA sequence of the mouse ABCG5 gene of the mouse ABCG5 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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nilarity 80.4%;
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Mismatches 403;
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                TGTAGTGGCTCTGCCGATTGCCGGGGGTGCTTGTTGGATCTGGATTCCTCAGAAACAT
                                                                              TGGTGAATTTCTAACTCTTGTGCTACTTGGTATCGTCCAAAATCCAAATATAGTCAACAG
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                                                                                                                                              ACATCCTGAGGTTGCCCGATTTGGATATTTTTCTGCTGCTCTCTTGGCCCCCCACTTAAT
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                                                                 Novel sitosterolemia susceptibility gene polypeptide and polynucleotide, useful for screening a compound that increases the level of expression or activity of SSG polypeptide for treating sterol-related disorder
                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                             Claim
                                                                                                                                                                                                                                 18-APR-2000;
15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sterol-related disorder; hyperlipidaemia; hypercholesterolaemia; therapy; gall stone; coronary heart disease; cardiovascular disease; arthritis;
                                                                                                                                                                                                        (TULA-)
                                                                                                                                                                                                                                                                       18-APR-2001; 2001WO-US12758
                                                                                                                                                                                                                                                                                                   25-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse sitosterolaemia susceptibility gene (SSG)
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invention relates to an isolated Sitosterolaemia Susceptibility polypeptide. SSG is a member of adenosine triphosphate (ATP)
                                                                                                                                     2002-017598/02
DB; AAE13289.
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                                        7; 105pp; English
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2000US-204234P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding cassette (ABC) family cholesterol transporter. SSG is useful for identifying a compound useful in the treatment or prevention of a
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      CTGCATGACTGCAAATCAAATTGTCCTTCTCTTGGCTGAGCTGGCTCGCAGGGACCGAAT
                         CTGCATGACTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTGGCTCGCAGGAACCGAAT
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Query Match Best Local Similarity

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Length 1959;

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                                                            The invention relates to ATP-binding cassette (ABC) family cholesterol transporter, ABCG8 polypeptides and polynucleotides. The invention also provides ABCG5 polypeptides and polynucleotides. ABCG5 gene is also known as sitosterolaemia susceptibility gene (SSG). Sequences of the invention are useful for treating or preventing sterol-related disorders such as sitosterolaemia, hyperlipidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis and nutritional deficiencies. They are also useful in gene therapy. The present sequence is mouse
                                                                                                                                                                                                                                                                                                             Claim 11; Page 73; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                            New ABCG8 polypeptides and nucleic acids, useful for treating sterol-related disorders e.g. sitosterolemia, hypercholesterolemia, hyperlipidemia, gall stones, HDL deficiency, atherosclerosis, or nutritional deficiencies -
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28-NOV-2000;
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1004 TRCTATATGGACCTGACGTCAGTGGATACCCAAAGCAAAG	884 TITGACAAAATIGCCATCCTGAGCTTCCGGAGAGCTGATTTTCTGTGGCACGCCAGCCGAA 943	764 ACCACAGGCCTGGACTGCATGACTGCTAATCAGATTGTCGTCCTGCTGGTGGAACTGGCT 823	703	84 21	404 TCCGGGAGGCTGCGCGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGC 463 [224 ATCCTCCATGCCTCCTACAGGTTCGGTCACGGGCACAGAGGCTCGGCACAGCTTAGGT 120 224 ATCCTCCATGCCTCCTACAGCGTCAGCCACCGCTGAGGCCCTGGTGGGACATCACATCT 283 121 GTCCTGCATGTCCTACAGCGTCAGCAACCGTGTGGGCCTTGGTGGAACATCAAAATCA 180 284 TGCCGGCAGGTGGACCAGGCAGGCATCCAAAAGATCTCTCTTGTACGTGGAGCGCGG 343	
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RESULT 8 ABK51686 ABK51686 XX AC ABK51686; XX DT 30-JUL-2002 (first entry) XX DE CDNA encoding rat ABCG5; protein. XX XX XX XX XX XX XX XX XX	7 1964 TTCACAATGAACTTTCTGATTTGTATTCCAGCTCTTGTCATCCTAGGAATA	1844 1741 1904 1801	1621 1784 1681	1501 1501 1664 1561	1381 1544 1441	1261 1424 1321 1484	1304 1201 1364	Qy 1184 GATTCTCCTGGAGTTTTCTCTAAACTGGGTGTTCTCCTGAGGAGAGTGACAAGAAACTTG

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                                                                                                                                                                                                                                                                                                           The present invention relates to a new mammalian ATP-binding cassette C gene 5 (ABCG5) polypeptide. The invention is useful for identifying a credisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell C culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal, CC where an increase or decrease in ABCG5 biological activity compared to CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal not CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 RNNA, or level of the CC polypeptide in a cell culture or mammal is also compared with that of a Second cell culture or mammal is also compared with that of a Stimulation of ABCG5 activity is useful for treating or preventing CC disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present nucleic acid sequence encodes the rat ABCG5 protein of the invention.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                     Sequence 2035 BP; 481 A; 533 C; 537 G; 484 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 45-46; 66pp; English.
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   CACATCTTGCCGGCAGCAGTGGACCAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGA 336
                                              CTTAGGTGTCCTGAATGTGTCCTTCAGCGTCAGCAACCGTGTCGGGCCCCTGGTGGAACAT
                                                              CCTGGGCATCCTCCATGCCTCCTACAGCGTCAGCCCACCGCGTGAGGCCCTGGTGGGACAT
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                                                                                                                                  AAACTTGGTGAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAGAATCTGATCATGGG
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                           GGACCGCGTAGGTCTCCTTTACCAGTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAA
                                                         TCTGTTCCTCATTTTCTACCTTCTCCGAGTCCAGAACAACATGCTGAAGGGCGCTGTTCA
                                                                                                                 AAACCTAATGAGGAATAAGCAGGTGGTGATTATGCGTCTTGTTCAGAATCTGATCATGGG
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                                                                                                                                                                                       Mus sp.
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                                                                                                                                                                                                                                                                                                                     mouse
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                                                                                               /*tag=
           /product- "Mouse ABCG5 protein"
/transl_except- (pos: 1912..1915, aa: LGIVIFKVRDYLISR)
/note- "This sequence lacks a stop codon"
                                                                                                                                             Location/Qualifiers
                                                                               /partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying a compound which alters ABCG5 activity level comprising contacting a cell CC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal. CC where an increase or decrease in ABCG5 biological activity compared to contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal not CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity, or level of ABCG5 mild type polypeptide. The CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the CC polypeptide in a cell culture or mammal is also compared with that of a second cell culture or mammal comprising a wild type ABCG5 polypeptide. CC iscases. The method of the invention is useful for treating or preventing construction and/or decreasing cholesterol adsorption. The present nucleic acid sequence encodes the mouse ABCG5 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 1560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1915 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel mammalian ATP-binding cassette gene 5 polypep nucleic acid encoding the polypeptide, useful for t sitosterolemia, arteriosclerosis and heart diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new mammalian ATP-binding cassette gene 5 (ABCG5) polypeptide. The invention is useful for identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200227016-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 42-43; 66pp; English.
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TCCGGGAGGCTGGGGCGCGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGCG
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81.5%;
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                                AATCTGTTTCCCGTGCTGCGAGCTGTCAGCGACCAGGAGGGGTCAGGACGGCCTCTACCAG
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                                              (USSH) US DEPT HEALTH (PATE/) PATEL S B. (DEAN/) DEAN M.
WPI; 2002-416483/44
P-PSDB; AAU96987.
                                                                                                                                                                                                                                                    Hamster; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol; arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
                            Patel SB,
                                                                                   25-SEP-2000; 2000US-235268P
                                                                                                                        04-APR-2002
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                                                                                                   25-SEP-2001; 2001WO-US29859
                                                                                                                                                                                                                                                                                  cDNA encoding hamster ABCG5
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/partial
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                                                                                                                                                          /product= "Hamster ABCG5 protein"
/note= "This sequence lacks both
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                                                                & HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The present invention relates to a new mammalian ATP-binding cassette CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a CC predisposition for developing sitosterolemia, arteriosclerosis or heart CC disease. The molecules of the invention are also useful for identifying CC acompound which alters ABCG5 activity level comprising contacting a cell CC culture or mammal which have ABCG5 polypeptide with a compound and CC measuring ABCG5 biological activity in the cell culture or in mammal, CC where an increase or decrease in ABCG5 biological activity compared to CC contacted with the compound, identifies a compound that increases or CC decreases ABCG5 activity respectively. The cell culture or mammal CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The CC polypeptide in a cell culture or mammal is also compared with that of a cecond cell culture or mammal is also compared with that of a cecond cell culture or mammal is useful for treating or preventing CC disease. The method of the invention is useful for increasing cholesterol CC excretion and/or decreasing cholesterol adsorption. The present nucleic acid sequence encodes the hamster ABCG5 protein of the invention.
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Best Local :
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CTCCAGGATCCTAAGGTCATGCTGTTTGATGAGCCAACCACAGGCCTGGACTGCATGACT
                       TTCGGAGAGCTGATTTTCTGTGGCACGCCAGCGGAAATGCTTGATTTCTTCAATGACTGC
                                                          ACCATTCACCAGCCCCGTTCTGAGCTTTTTCAGCTCTTTGACAAAATTGCCATCCTGAGC
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ULT 11 22022 AAD22022 standard; DNA; 472 BP.

Human sitosterolaemia susceptibility gene (SSG) exon 13

12-FEB-2002

(first entry)

Human; sitosterolaemia susceptibility gene; SSG; atherosclerosis; sterol-related disorder; hyperlipidaemia; hypercholesterolaemia; therapy; gall stone; coronary heart disease; cardiovascular disease; arthritis; xanthoma; haemolytic anaemia; transgenic animal; ds.

Homo sapiens.

N W0200179272-A2 X D 25-OCT-2001.

18-APR-2001; 2001WO-US12758

18-APR-2000; 2000US-198465P. 15-MAY-2000; 2000US-204234P.

(TULA-) TULARIK INC

Tian H, Schultz J, Shan B;

R WPI; 2002-017598/02

Novel sitosterolemia susceptibility gene polypeptide and polynucleotide, useful for screening a compound that increases the level of expression or activity of SSG polypeptide for treating sterol-related disorder

Claim 73; Fig 14B; 105pp; English.

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sterol-related disorder, including sitosterolaemia, hyperlipidaemia, hyperlipidaemia, pall stones, HDL deficiency, atherosclerosis or nutritional deficiencies. SSG is also useful for treating cholesterol-associated diseases or conditions including coronary heart disease and other cardiovascular diseases, and sitosterolaemia-associated condition including arthritis, xanthomas and chronic haemolytic anaemia. SSG expression cassette is useful in the production of transgenic non-human animals. SSG genes and their homologues are useful as tools for a number of applications including diagnosing sitosterolaemia and other cardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The present sequence is an exon of human SSG DNA.
                   hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                     vulnerary; antipsoriatic; antiparkinsonian;
anticonvulsant; osteopathic; antiarthritic;
                                                                                                                                   vulnerary;
                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                    08-FEB-2001
                                                                            immunostimulant; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated Sitosterolaemia Susceptibility Gene (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) binding cassette (ABC) family cholesterol transporter. SSG is useful for identifying a compound useful in the treatment or prevention of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                  ORFX ORF1620 polynucleotide sequence SEQ ID NO:3239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                               open
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGTCTTTTAACCATTAAGACTCCATTTGTGCCTCTTGGATCCAAGCAGGCCTTGAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTCATTTATTCCAGCTCTTGTCATCCTAGGAATAGTTGTTTTCAAAATAAGGGATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGGAAGTGGTTTATAGTCCCTTGCTCTTACAACTTGCAGGGACATGTGGTTATTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATTAGCAGGTAGTGAAAGCCATGGCTGGGAAAATGGAAGTGAAGCTGCCGACTGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATTAGCAGGTAGTGAAAGCCATGGCTGGGAAAATGGAAGTGAAGCTGCCGACTGTGCA
                                                                                                                                   n reading frame; ORFX; detection;
antipsoriatic; antiparkinsonian;
                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 A; 93 C; 100 G; 145 T; 0 other;
  therapy;
                                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.2%; Score 472; DB 24; 100.0%; Pred. No. 1.2e-12
                                                                                                                                                                                                                                                                                                                                                                       432
  cancer;
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                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                       ntiarthritic; immunosuppressant; cardiant; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
proliferative
                                                                                                                      cytostatic; hepatotropic;
nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
hypertension;
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                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                        coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 2444; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; a cholesterol ester storage; systemic lupus erythematosus; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP
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                                                                     61
                                                                                                                                                                                                                430;
                                                                                                                                                                                                                               Similarity
                                                                                 AGAAACTTGGTGAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAGAATCTGATCATG
                                                                                                                                                                                                                                                                                       432
                          GGTTTGTTCCTCCTTTTCTTCGTTCTGCGGGTCCGAAGCAATGTGCTAAAAGGGTGCTATC
                                                              AGAAACTTGGTGAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAGAATCTGATCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA,
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contraceptive;
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                                                                                                                                                                                                                                                                                      BP; 87
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99US-0127728
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                                                                                                                                                                                                                                                                                                                  inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                  A; 110 C; 118 G; 117 T;
                                                                                                                                                                                                                           18.4%;
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                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                              Score 429.4;
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                                                                                                                                                                                                                               No.
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                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                  0 other;
                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                              Length 432;
                                                                                                                                                                                                          0;
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                               Query Match
Best Local :
       Best Local Similarity
Matches 279; Conser
                                                                                                                                                                    The present sequence is that of human ATP binding cassette (ABC) cDNA fragment 168043, identified as a cholesterol-sensitive gene fragment. The invention provides cholesterol-sensitive ABC genes (see AAZ94734-63). These genes, and polypeptides encoded by them, can be used for diagnostic and therapeutic applications, and for blochemical or cell-based assays to screen for pharmacologically active modulator compounds useful for the treatment of lipid disorders, atherosclerosis or other inflammatory diseases such as
                                                                                                           Sequence 281
                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenosine triphosphate binding proteins useful for identifying agents for treating atherosclerosis and other inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmitz G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP binding cassette; human; cholesterol; lipid disorder; atherosclerosis; lipid disorder; dyslipidemia; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ATP binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200018912-A2
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                                                                                                                                                                                                                                                                                                                                                                                                      9; Page 135; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erythematosus;
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                                                                                                                                                  and lupus erythematosus.
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       Conservative
                                                                                                        BP; 60
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                            11.5%;
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                       Score 268; DB 21;
Pred. No. 4.8e-64;
                                                                                                   73 G;
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     Mismatches
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Gaps

The present invention relates to a new mammalian AFP-binding cassette gene 5 (ABCC5) polypeptide. The invention is useful for identifying a predisposition for developing sitosterolemia, arteriosclerosis or heart disease. The molecules of the invention are also useful for identifying a compound which alters ABCC5 activity level comprising contacting a cell culture or mammal which have ABCC5 polypeptide with a compound and measuring ABCC5 biological activity in the cell culture or in mammal, where an increase or decrease in ABCC5 biological activity compared to ABCC5 biological activity in a control cell culture or mammal not contacted with the compound, identifies a compound that increases or decreases ABCC5 activity respectively. The cell culture or mammal compounds activity respectively. The cell culture or mammal activity respectively. The cell culture or mammal activity respectively or a wild type polypeptide. The ABCC5 biological activity, or level of ABCC5 mRNA, or level of the polypeptide in a cell culture or mammal is also compared with that of a

Example 3; Page 38-41; 66pp; English.

treating

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                                                                                                                                                                                                                                                                                                                                                                                                                    Novel mammalian ATP-binding cassette gene 5 polypeptide, nucleic acid encoding the polypeptide, useful for treatile sitosterolemia, arteriosclerosis and heart diseases -
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chromosome 2p21; o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patel SB,
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(PATE/) PATEL S
(DEAN/) DEAN M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ABCG5 upstream genomic
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                                Novel sitosterolemia susceptibility gene polypeptide and polypucleotide, useful for screening a compound that increases the level of expression or activity of SSG polypeptide for treating
Claim 73; Fig 14B; 105pp; English
                                                                                                                          Tian H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        second cell culture or mammal comprising a wild type ABCG5 polypeptide. Stimulation of ABCG5 activity is useful for treating or preventing hypersterolemia, arteriosclerosis, heart disease.and/or Alzheimer's disease. The method of the invention is useful for increasing cholesterol excretion and/or decreasing cholesterol adsorption. The present nucleic acid sequence represents the upstream genomic sequence, exon 1, intron 1 and exon 2 of the human ABCG5 gene located on chromosome 2p21.
                             sterol-related disorder
                                                                                               WPI; 2002-017598/02.
                                                                                                                                                    (TULA-) TULARIK INC
                                                                                                                                                                                                                                                                                                                                                   sterol-related disorder; hyperlipidaemia; hypercholesterolaemia; therapy;
                                                                                                                                                                                                                                                                                                                                                                   Human; sitosterolaemia susceptibility gene; SSG; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                              Human sitosterolaemia susceptibility gene (SSG) exon 1.
                                                                                                                                                                                                                                                  25-OCT-2001.
                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                 xanthoma; haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD22010 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5460 BP; 1351 A; 1350 C; 1508 G; 1243 T; 8 other;
                                                                                                                                                                               18-APR-2000;
15-MAY-2000;
                                                                                                                                                                                                                      18-APR-2001; 2001WO-US12758.
                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2002
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2000US-204234P.
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                                                                                                                       Shan B;
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98.4%;
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                                                                                                                                                                                                                                                                                                                                        disease; cardiovascular disease; arthritis;
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Pred. No. 3.8e-58;
                                                                                                                                                                                                                                                                                                                               transgenic
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Mismatches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SSG) polypeptide. SSG is a member of adenosine triphosphate (ATP) binding cassette (ABC) family cholesterol transporter. SSG is useful for identifying a compound useful in the treatment or prevention of a sterol-related disorder, including sitosterolaemia, hyperilpidaemia, hypercholesterolaemia, gall stones, HDL deficiency, atherosclerosis or nutritional deficiencies. SSG is also useful for treating cholesterol-associated diseases or conditions including coronary heart disease and other cardiovascular diseases, and sitosterolaemia-associated condition including arthritis, xanthomas and chronic haemolytic anaemia. SSG expression cassette is useful in the production of transgenic non-human animals. SSG genes and their homologues are useful as tools for a number of applications including diagnosing sitosterolaemia and other cardiovascular diseases for foreneirs and naternity determinations.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 249 BP; 44 A; 86 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disorders, for forensics and paternity determinations, and for treating any of a large number of SSG associated diseases. The present sequence is an exon of human SSG DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated Sitosterolaemia Susceptibility Gene
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                                CAGCGTCAG 249
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CAGCGTCAG 249
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                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 8.6e-59;
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Search completed: July 27, 2003, 00:55:32 Job time: 570.197 secs

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Minimum DB
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2003 Compugen Ltd
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Match 186091 472 127066 139342 2809 Length DB 10 10 AC084265 AC108476 F351812S01 AF404106 AX456521 AR404107 Homo sapi AC084712 Homo sapi AX320893 Sequence AX320894 Sequence AF320894 Homo sapi AX685735 Sequence AF324494 Homo sapi AY196215 Mus muscu AY196216 Mus muscu AY196216 Mus muscu AY196216 Mus muscu AY196216 Mus muscu AY196216 Mus muscu AY196216 AY10 Muscu AY196216 AY10 Muscu AY196216 Mus muscu AY196216 AY10 Muscu AY196216 Mus muscu AY196216 Mus muscu AY196217 Rattus no AC120701 Rattus no AC112747 Rattus no AC093410 Oryctolag AP001111 Oryca sat AC084405 Oryza sat AX456520 Sequence AX456519 Sequence AX195873 Mus muscu AX456524 Sequence AX320881 Sequence AF312714 Rattus no AX320883 Sequence AX685733 Sequence Description AF312713 Mus muscu AY195872 Mus muscu 11997 Homo sapi 16528 Sequence 1242 Homo sapi Sequence Sequence Sequence Sequence Homo sap Sequence Sequence

ALIGNMENTS

TITLE	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX320883
Sitosterolemia susceptibility game (seq): compositions and extra		Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi	Homo sapiens	Homo sapiens (human)		·AX320883.1 GI:17902433	AX320883		AX320883 /2340 bp DNA linear DAT 14-DEC-2001	`

Pred. No.

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Best Local Similarity 100.0%;
Matches 2340; Conservative
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                                     CGAGACGCTGCACTACACCGCGCTGCTGGCCATCCGCCGGCGCAATCCCGGCTCCTTCCA
                                                            CCAGGACTGCTTCTCCTACGTCCTGCAGAGCGACCACCCTGCTGAGCAGCCTCACCGTGCG
                                                                                                         CGCGGGGACCTTCCTGGGGGAGCTGTATGTGAACGGCCGGGCGCTGCGCCCGGGAGCAGTT
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                CGAGACGCTGCACTACACCGCGCTGCTGCCCATCCGCCGCGCAATCCCGGGCTCCTTCCA
                                                                                                                                                     AGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCG
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//db_xref="GI:17902434"
//db_xref="GI:17902434"
//db_xref="GI:17902434"
//translation="McDLSSLTPGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHAS
/*translation="McDLSSLTPFGGSMGLQVNRGSQSSLEGAPATAPEPHSLGILHAS
/*translation="McDLSSLTPFGGSMGLQVNRGSQSSCKTTLLDANSGR
ISVSHRVRPWNDITSCRQQWTRQILKDVSLYVLGSDTLLSGITVRETLHYTALLAIRGN
IGSRQKVEAVMAELSLSHVADALLIGNYGISTGERRRVSIAAQLLQDFKVMLFDE
PTGLDCMTANQIVVLLVELARRNRIVVLTIHOPRSELFQLFDKTALLSFGELFQCF
PAEMLDFFNDCGYPCPEHSNPPDFYMDLTSVDTQSKBREIETSKRVQMIESAYKKSAI
CHKTLKN IERMKHLKTLPMVPFKTKDSPGVFSKLGVLLRRYTRNLVRNKLAVITRLLQ
NLIMGLFLLFFVLRVBSNVLKGAIQDRYGLLYQPVGRJPYTGMLANVNLFPVLRAVSD
QESQDGLYQKNQMMLAYALHYLPFSVVATMIESSVCYWTLGLHPEVARFGYFSAALLA
PHLIGEFLTLVLLGIVQNPNIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIISYFT
FQKYCSEILVVNEFYGLNRTCSSNVSYTTNPMCAFTQGIQFIEKTCPGATSRFTMNF
LILYSFTPALVILGIVFKIRDHLISR"
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Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/mol_type-"genomic DNA"
/db_xref-"taxon:9606"
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9	GGTTCTCACCATTCACCAGCCCCGTTCTGAGCTTTTTCAGCTCTTTGACAAAATTGCCAT 900 	CATGACTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTGGCTCGCAGGAACCGAATTGT 840	CCAGCTGCTCCAGGATCCTAAGGTCATGCTGTTTGATGAGCCACACAGAGGCCTGGACTG 780 [[TGGCAACTACAGCTTGGGGGGCATTTCCACGGGTGAGCGGCGCCGGGTCTCCATCGCAGC 720	GAAGAAGGTGGAGGCCGTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGAT 660	CGAGACGCTGCACTACACCGCGCTGCTGGCCATCCGCCGGGCAATCCCGGCTCCTTCCA 600	CCAGGACTGCTTCTCCTACGTCCTGCAGAGCGACACCCTGCTGAGCAGCCTCACCGTGCG 540	CGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGCGCTGCGCCCGGGAGCACTT 480	AGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCG 420	CAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGGGGGCAGATCATGTGCATCCT 360	CAGCGTCAGCCACCGCGTGAGGCCCTGGTGGGACATCACATCTTGCCGGCAGCAGTGGAC 300	GGAGGGGGCTCCTGCCACCGCCCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTA 240		GGGTCCGGCCACCAGAAAATTTGCCCAGCTTTGCTGCCTGTTGGCCATGGGTGACCTCTC 120 	1 GTCAGGTGGAGCAGGCAGGCAGTCTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGA 60 	h . 100.0%; Score 2340; DB 9; Length 2340; Similarity 100.0%; Pred. No. 0; 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	541 a 601 c 598 g 600 t	NLIMGLELLEFVLRVRSNYLKGAIODRVGLLYOFVGATPYTGMLNAVNLEPVLRAVSD QESODGLYOKWOMMLAYALHVLPFSVVATMIFSSVCYWTLGLHDEVARFCYFSAALLA PHLIGEFLTIVLLGIVQNPNIVNSVVALLSIAGULVGSSBLRNIQEMPIPFKIISYFT
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1981 GATTTTGTATTCATTTCCAGCTCTTGTCATCCTAGGAATAGTTGTTTTCAAAATAAG 2040	1921 AATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAGATTCACAATGAACTTTCT 1980 	1861 CACTTGTGGCAGCTCAAATGTTTCTGTGACAACTAATCCAATGTGTGCCTTCACTCAAGG 1920 	1801 TACATTCCAAAAATATTGCAGTGAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTT 1860	1741 ATCTGGATTCCTCAGAAACATACAAGAAATGCCCATTCCTTTTAAAATCATCAGTTATTT 1800 	1681 AAATCCAAATATAGTCAACAGTGTAGTGGCTCTGCTGCTGCAATGCGGGGGTGCTTGTTGG 1740	1621 TCTCTTGGCCCCCCACTTAATTGGTGAATTTCTAACTCTTGTGCTACTTGGTATCGTCCA 1680			1441 GCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGAAGTGGCAGATGATGCT 1500 	1381 GTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAACGCTGTGAATCTGTTTCCCGTGCT 1440		1261 AGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTTTCTTCGTTCT 1320	1201 CTCTAAACTGGGTGTTCTCCTGAGGAGAGTGACAAGAAACTTGGTGAGAAATAAGCTGGC 1260 	1141 GAAACACCTGAAAACGTTACCAATGGTTCCTTTCAAAACCAAAGATTCTCCTGGAGTTTT 1200 	1081 AGAATCTGCCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAAT 1140 	1021 GTCAGTGGATACCCAAAGCAAGGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGAT 1080 	961 TGACTGCGGTTACCCTTGTCCTGAACATTCAAACCCTTTTGACTTCTATATGGACCTGAC 1020	

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20578753
                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-OCT-2000) Division of Endocrinology, Diabetes Medical Genetics, Medical University of South Carolina, 114 st, STB541, Charleston, SC 29403, USA on Jun 14, 2001 this sequence version replaced gi:12382303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens sterolin (ABCG5) mRNA, AF312715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

A (bases 1 to 2740)
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Direct Submission
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YSVSHRVRPWWDITSCRQQWTRQILKDVSLTVESGQIMCILGSSGSGKTTLLDAMSGR
YSVSHRVRPWWDITSCRQQWTRQILKDVSLTVESGANGLLQDPXVMLFDE
PGSFQKKVEAVMAELSLSHVADRLICNYSLGGISTGERRKYSIAAOLLQDPXVMLFDE
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             PTTGLDCMTANQIVVLLVELARRNRIVVLTIHQPRSELFQLFDKTAILSFGELIFGGT
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tissue_type="liver"
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, Pegoraro, R., Srivastava, A.K.,
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NLIMGLELLEFVLRVRSNVLKGAIQDRVGLLYQFVGATPYTGMLNAVNLFPVLRAVSD
QESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLA
PHLIGEFLILVLLGIVQRFNIVNSVVALLSIAGVLYGSGFLRNIQEMPIPFKIISYFT
FQKYCSEILVVNEFYGLNFTCGSSNVSVTTNPMCAFTQGIQFIEKTCPGATSRFTMNF
LILYSFIPALVILGIVFKIRDHLISR*

669 a 670 c 702 g 699 t

100.0%; Score 2340. DB 9. Leagth 2740.
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### Best Local Similarity 100.00; Poll No.00; Poll Marches 240; Conservative 0; Hismatches 0; Indels 0; Gaps 1 111111111111111111111111111111111	960	CCTGAGCTTCGGAGAGCTGATTTTCTGTGGCACGCCAGCGGAAATGCTTGATTTCTTC	ō .	~
Matches 2340; Conservative 0, Hismatches 0, Index 1, Lenyth 2740; Matches 2340; Conservative 0, Hismatches 0, Index 1, 100; Gaps 1, 10		1 GGTTCTCACCATTCACCAGCCCCGTTCTGAGCTTTTTCAGCTCTTTGAGAAAATTGCCAT	7	₽. ₩
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Best Local Similarity 100.0%; Pred. 0.0; Matches 2340; Conservative 0; Mismatches 0; Indels 0; Gaps 1 GTCAGGTGGAGCAGGCAGGCAGGTCTGCCACCGGGCTCCCCAACTGAAGCCACTCTGGGGA	18	1 ATCTTTGACCCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCC		7
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Sequence 42 from Patent
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                                                                         ATCTTTGACCCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCT
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863 CGTTCTGAGCTTTTTCAGCTCTTTGACAAAATTGCCATCCTGAGCTTCGGAGAGCTGATT 922 	803 GTCCTCCTGGTGGAACTGGCTCGCAGGAACCGAATTGTGGGTTCTCACCAGTCACCAGCCC 862	743 GTCATGCTGTTTGATGAGCCAACCACAGGCCTGGACTGCATGACTGCTAATCAGATTGTC 802	83 ATTICAACGGGTGAGCGGCGCGGGTCTCCATCGCAGCCCAGCTCCAGGATCCTAAG 742	23 GCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGATTGGCAACTACAGCTTGGGGGGGC 682	63 CTGCTGGCCATCCGCCGCGCAATCCCGGCTCCTTCCAGAAGAAGGTGGAGGCCGTCATG 622 	103 CTGCAGAGCGACACCCTGCTGAGCAGCCTCACCGTGCGCGAGACGCTGCACTACACCGCG 562	443 GTGTATGTGAACGGCCGGGCGCTGCGCCGGGAGCAGTTCCAGGACTGCTTCTCCTACGTC 502	383 ACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCGCGCGGGGACCTTCCTGGGGGAG 442	323 TCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAAA 382	263 CCCTGGTGGGACATCACATCTTGCCGGCAGCAGTGGACCAGGCAGATCCTCAAAGATGTC 322	203 CCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTACAGCGTCAGCCACCGCGTGAGG 262	143 ATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCTGGAGGGGGCTCCTGCCACCGCC 202 	tch 82.1%; Score 1920; DB 6; Length 1920; al Similarity 100.0%; Pred. No. 0; 1920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/w_^.ce_	e 1.1920 organism="synthetic construct" /mol_type="genomic DNA" /Ab vef="tyon.23620"	~ ~	artificial sequences. 1 Patel,S.B. and Dean,M. Gene involved in dietary sterol absorption and excretion and uses therefor
Qy Qy	ОУ	Оy	Db Qy	Qy Db	Qy	Qy dd	da Vo	Qγ	ОУ	ОУ	ОУ	Оy	Оy	Db Qy	Оу	Qу	Фу
1943 TGCCCAGGTGCAACATCTAGATTCACAATGAACTTTCTGATTTTGTATTCATTTATTCCA 2002	83 41	1823 GAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTTCACTTGTGGCAGCTCAAATGTT 	1763 CAAGAAATGCCCATTCCTTTTAAAATCATCAGTTATTTTACATTCCAAAAATATTGCAGT 	1703 GTAGTGGCTCTGCTGTCCATTGCGGGGGTGCTTGTTGGATCTGGATTCCTCAGAAACATA	43 01	1583 CATCCTGAGGTTGCCCGATTTGGATATTTTTCTGCTGCTCTTGTGCCCCCCCACTTAATT	23 81	1463 AGTCAGGACGGCCTCTACCAGAAGTGGCAGATGATGCTGGCCTATGCACTGCACGTCCTC	1403 ACAGGCATGCTGAACGCTGTGAATCTGTTTCCCGTGCTGCGAGCTGTCAGCGAGCAGGAG	1343 AAGGGTGCTATCCAGGACCGCGTAGGTCTCCTTTACCAGTTTGTGGGGGCCCACCCCGTAC	1283 AATCTGATCATGGGTTTGTTCCTCCTTTTCTTCGTTCTGCGGGTCCGAAGCAATGTGCTA 	1223 AGGAGAGTGACAAGAAACTTGGTGAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAG 	1163 ATGGTTCCTTTCAAAACCAAAGATTCTCCTGGAGTTTTCTCTAAACTGGGTGTTCTCCTG	1103 GCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAATGAAACACCTGAAAACGTTACCA 	1043 GAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGATAGAATCTGCCTACAAGAAATCA 1102 	983 GAACATTCADACCCTTTTGACTTCTATATGGACCTGACGTCAGTGGATACCCAAAGCAAG	

AATGGTTCCTTTCAAAACCAAAGATTCTCCTGGAGTTTTCTCTAAACTGGGTGTTCTCCT 	Qy Db	57 CTCCCATTGGCTCAGTTAAAGCTGCCCTGGAGCCGGACAGGCCACTAGAAAATTCAC 116 85 CCAGCTTTGCTGGCCATTGGGCATGACCTCTCATCTTTGACCCCCGGAGGGTCCAT 144	Qy ,
1102 AGCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAATGAAACACCTGAAAACGTTACC 1161 	Qy	CTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGGAGGGTCCGGCCACCAGAAAATTTGC	P 49
1042 GGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGATAGAATCTGCCTACAAGAATC 1101 	дь	Query Match 60.3%; Score 1410.8; DB 10; Length 2351; Best Local Similarity 80.4%; Pred. No. 1.4e-296; Matches 1665; Conservative 0; Mismatches 402; Indels 3; Gaps 1;	Quer Best Matc
	Db	BASE COUNT 569 a 605 c 594 g 583 t ORIGIN	BASE C
957 GTTCTGTGGCACCCCAGAGGAGATGCTTGGCTTCTTCAATAACTGTGGTTACCCCTGTCC 1016	Qy Qy	DQESQDGLYHKWQMLLAYVLHVLPESVIATVIFSSVCYWTLGLYPEVARFGYFSAALL APHLIGEFLTLVLLGIVQNPNIVNSIVALLSISGLLIGSGFIRNIQEMPIPLKILGYF TFQKYCCEILVVNEFYGLNFTCGGSNTSMLNHPMCAITQGVQFIEKTCPGATSRFTAN	
922 TTTCTGTGGCACGCCAGCGGAAATGCTTGATTTCTTCAATGACTGCGGTTACCCTTGTCC 981	Qy	IYHKILENIERARYLKTLPTVPFKTKDPPGMFGKLGVLLRRVTRNLMRNKQAVIMILV QNLIMGLFLIFYLLRVQNNTLKGAVQDRVGLLYQLVGATPYTGMLNAVNLFPMLRAVS	
862 CCGTTCTGAGCTTTTCAGCTCTTTGACAAATTGCCATCCTGAGCTTCGGAGAGCTGAT 921	Фр	SADE'NKKVEAVMTELSLISHRADATIOETSI VAGJUVELJSLIT KETILKITAMLALICKS SADE'NKKVEAVMTELSLISHRADATIGSYNFGGI SSGERRRYSI AAQLIQDRKVMALD EPTTGLICMTANQI VLLLABELARRDRI VI VITIHQPRSELFETYKRYOMI, PCARK RSD TPEEMIGEFUNGGY PCPEHSNPFDEYMOLTSVOTOSREREI ETYKRYOMI, PCARK RSD	
	DЪ	/translation="MGELPFLSPEGARGPHINRGSLSSLEQGSVTGTEARHSLGVLHV SYSUSNRVGPWNNIKSCQKWDRQILKDVSLYIESGQIMCILGSSGSGKTTLLDAISG	
802 CGTCCTCCTGGTGGAACTGGCTCGCAGGAACCGAATTGTGGTTCTCACCATTCACCAGCC 861	Qy	Hellerer	
77 GETCATGATGATGAGCCACACCACGACTGCACTGCATGACTGCTAATCAGATTGT 801	₽ <i>\$</i>	white subfamily" /codon_start=1 /product="ayrp-hinding cassette sub-family G member 5"	
AATTTCCAGTGGGGGGCGCGAGTTTCCATCGCAGCCCAACTCCTTCAGGACCCCAA	2 5		
CATTICCACGGGTGAGCGGCCCGGGTCTCCATCGCAGCCCAGCTGCTCCAGGATCCTAA	P 09	/gene_Abcg5" CDS 139. 2097	o 4
57	рb	/sex="male" /tissue_type="liver" 2151	٥
622 GCCAGAGCTGAGCCATGTGGCAGACCGACTGATTGGCAACTACAGCTTGGGGGG 681	Qy	/chromosome="17" /map="55_cM"	·
597. GATGCTGGCCCTCTGCCGCAGCTCCGCGGACTTCTACAACAAGAAGGTAGAGGCAGTCAT 656	Db	/strain="pera/gi" /db_xref="taxon:10090"	
562 GCTGCTGGCCATCCGCCGCGGCAATCCCCGGCTCCTTCCAGAAGAAGGTGGAGGCCGTCAT 621	Qy ·	/mo	
	Db	Bar Harbor, ME 04609, U Location/Quali rce 12351	FEATURES Sou
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442 GGTGTATGTGAACGGCCGGGGGGCGCTGCGGGGAGCAGTTCCAGGACTGCTTCTCCTACGT 501	Qy Db		JOURNAL REFERENCE AUTHORS
417 GACCACGCTGCTGGACGCCATCTCCGGGAGGCTGCGGCGCACTGGGACCCTGGAAGGGGA 476	Db		TITLE
	Q 5	Wittenburg Paigen, B.	AUTHORS
22 CTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAA	py Oy		REFERE
	Db	URCE Mus musculus (house mouse) ORGANISM Mus musculus	SOURCE ORGANI
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205 GGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTACAGCGTCAGCCACCGCCGTGAG 261	ФЪ	Z	DEFINI
177 AGGGCCTCACATCAACAGAGGGTCTCTGAGCTCCCTGGAGCAAGGTTCGGTCACGGCCAC 236	Фф		RESULT 7 AY195873
	Qy ·	1861 GCTCTTGTCATCCTAGGAATAGTTGTTTTCAAAATAAGGGATCATCTCATTAGCAGGTAG 1920	Db
117 TTGCATTTGCTTCCTGCTAGCCATGGGTGAGCTGCCCTTTCTGAGTCCAGAGGGAGCCAG 176	Db.		ļ

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AF312713.2 GI:14091944
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Nat. Genet. 27 (1), 79-83 (2001)
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Direct Submission
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Lyons,M.A., Wittenburg,H., Walsh,K.A., Carey,M.(
Direct Submitted (11-DEC-2002) The Jackson Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 2351)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus strain I/LnJ ATP-binding cassette sub-family G member 5 (Abcg5) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wittenburg, H., Lyons, M.A., Li, R., Churchill, G.A., Carey, M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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             CCAGCTTTGCTGCCTGTTGGCCATGGGTGACCTCTCATCTTTGACCCCCGGAGGGTCCAT
                                        CTCCCATTGGCTCAGTTAAAGCTGCCCTGGAGGCCGACAGCCACTAGAAAATTCAC
                                                                    CTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGAAGGGTCCGGCCACCAGAAAATTTGC
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TPEEMLGFFNNCGYPCPEHSNPFDFYMDLTSVDTQSREREIETYKRVQMLESAFKESD
IYHKILENIERARYLKTLPTVPFKTKDPPGMFCKLGVLLRRVTKNLMRNKQAVIMRLV
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RLRCTGTLEGDVFVNGCELRRDOFQDCFSYVLOSDVFLSSLTVRETLRYTAMLALCRS
SADFYNKKVEAVMTELSLSHVADQVIGSYNFGGISSGERRRVSIAAQLLQDPKVNMLD
                                                                                                                                                                                                                                                                                                                                                /product="ATP-binding cassette sub-family G member 5"
/protein_id="AAO45093.1"
/db_xref="GI:31322256"
/translation="MGELPFLSPEGARGPHINRGSLSSLEQGSVTGTEARHSLGYLHV
                                                                                                                                                                                                                                                                                                                                                                                                                                  white subfamily"
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Mus musculus
Eukaryota; Metazoa; Chorda
                                   AX320881 2258 bp
Sequence 2 from Patent W00179272
AX320881 GI:17902431
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                                                                                                    GTTAAGATGACAGGCAGGAAAGGGTTAATG
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  Craniata;
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/PIOLEIN_id="CAD19408.1"
//db xref="GI:17902432"
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//translation="MGELPFLSPEGARGPHINRGSLSSLEQGSVTGTEARHSLGVLHV
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SYSVSRRVGPWWNIKSCQQKWDRQILKDVSLYIESGQIMCILGSSGSGKTTLLDAISG
RLRRTGTLEGEVFVNGCELRRDQFQDCFSYVLQSDVFLSSLTVRETLRYTAMLALCRS
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EPTTGLDCMTANQIVLLLAELARRDRYVTYTHQPFSELFQHFDKIAILTYGELVFCG
TPEEMLGFFNNCGYPCPEHSNPFDFYMDLTSVDTQSREREIETYKRVQMLECAFKESD
IYHKILENIERARYIKKTLPMVPFKTKDPPMFGKLGVLGATPYTGHLNAVNLFPMLRAVS
QULINGLFLEFYLRVQNNTLKGAVQDTVGATPYTGHLNAVNLFPMLRAVS
DQESQDGLYHKWQMLLAYVLHYLPFSVLATVIESSVCYMTLGIVEVARRGYFSAALL
APHLIGEFLINVLGIVONDRIVNSIVALLSIGGLIGGSFIRNIQEMFIPLKILGYF
TFOKYCCELLVVNEFYGLNDTTCGGSNTSMLNHPMCAITQGVQFIEKTCPGATSRETAN
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/mol_type="genomic DNA"
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Score 1395.6; DB 6; Pred. No. 2.8e-293; 0; Mismatches 389; Indels Length ω •• Gaps ۲.

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CTACAGCGTCAGCCACCGCGTGAGGCCCTGGTGGGACATCACATCTTGCCGGCAGCAGTG

GACCAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCAT

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CTTAGGCAGCTCAGGGAAGACCACGCTGCTGGACGCCATCTCCGGGAGGCTGCG CCTAGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGG 417 360

GCGCGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGCCCTGCGCCCGGGAGCA GTTCCAGGACTGCTTCTCCTACGTCCTGCAGAGCGACCCCTGCTGAGCAGCCTCACCGT GCGCACTGGGACCCTGGAAGGGGAGGTGTTTGTGAATGGCTGCGAGCTGCGCAGGGACCA 537 420 477

GCGCGAGACGCTGCACTACACCGCGCTGCTGGCCATCCGCCGCGGCAATCCCGGCTCCTT GTTCCAAGACTGCTTCTCCTACGTCCTGCAGAGCGACGTTTTTCTGAGCAGCCTCACTGT 597 54 C 480

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Medical Genetics, Medical University of South Carol St, STB 541, Charleston, SC 29403, USA Sequence update by submitter On Aug 26, 2002 this sequence version replaced gi:10 Location/Qualifiers
                                                                                 Lu,K., Lee,M. and Patel,S.B.
Direct Submission
Submitted (26-AUG-2002) Division
                                                                                                                              Sequence update by submitter 4 (bases 1 to 2470)
                                                                                                                                                       Medical Genetics, Medical University of South St, STB 541, Charleston, SC 29403, USA
                                                                                                                                                                                                      Lu,K., Lee,M.-H. and Patel,S.B
Direct Submission
                                                                                                                                                                                                                                Submitted (12-OCT-2000) Division of Endocrinology, Diabetes Medical Genetics, Medical University of South Carolina, 114 St. STB 541, Charleston, SC 29403, USA (bases 1 to 2470)
                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 2470)
Lee, M.H., Lu,K., Hazard,S., Yu,H., Shulenin,S.
Kojima,H., Allikmets,R., Sakuma,N., Pegoraro,F
Salen,G., Dean,M. and Patel,S.B.
Identification of a gene, ABGG5, important in
dietary cholesterol absorption
dietary Genet. 27 (1), 79-83 (2001)
                                                                                                                                                                                      Submitted (16-MAY-2001)
                                                                                                                                                                                                                                                                                             Lu,K., Lee,M.-H. and Patel,S.B. Direct Submission
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Mammalia; Eutheria;
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Query Match 58.4%; Score 1365.4; DB 6; Length 1959; Best Local Similarity 81.4%; Pred. No. 1e-286; Matches 1595; Conservative 0; Mismatches 361; Indels 3; Gaps 1;	APHLIGEFUTUVLIGIVQNPNIVNSIVALLSISGLLIGSGFIRNIQEMPIPLKILGYF TFQKYCCEILVVNEFYGLNFTGGSWTSMLNHPMCAITQGVQFIEKTCPGATSRFTAN FLILVGFIFALVILGIVJFKVRDYLISR* BASE COUNT 468 a 506 c 495 g 490 t ORIGIN	TPEEMIGFFUNGG FOODERSNOWN TO THINK ROBIN FOR THAILI I GENT FOODERSNOWN TO THE CONTROL OF THE PROPERTY OF THE P	RLRRTGTLEGEFFVNGCELRRDQFQDCFSYTLQSDFQLStTVRETLRYTAMLALCRS SADFYNKKVEAVWTELSLSHVADQWIGSYNFGGISGGERRRVSIAAQLLQDFKVMMLD EPTTGLDOWTANOIVLLLAFLARBRRIVIVTTHOODSET.FOHFDR TAILTVCET VECC	/protein_id="CAD86570.1" /db_xref="GI:29371739" /translation="MGELPPISPEGARGPHINRGSLSSLEQGSVTGTEARHSLGVLHV SYSYSNRVGPWWNIKSCOOKWDROTTKNVSLYTEGGOTWGTIGSGGGGGTTTTTTATGG	CDS /GD_XFEI="taxon:10090" 1. 1959 /note="unnamed protein product; ABCG5 (mABCG5)" /codon_start=1	FEATURES LOCATION/Qualifiers Source 11959 /organism="Mus musculus" /mol_type="genomic DNA"	JOURNAL Patent: WO 02081691-A 1 17-OCT- Tularik Inc. (US); BOARD OF RE (US)	EUKAIYOTA; Metazoa; Chordata; Craniata; Ye Mammalia; Eutheria; Rodentia; Sciurognath; CE 1 RS Hobbs, H.H., Shan, B., Barnes, R. and Tian, H.	S Mus musculus (house mouse) ISM Mus musculus	AX685729 LOCUS AX685729 DEFINITION Sequence 1 from Patent WO02081691. ACCESSION AX685729 VERSION AX685729 AX685729 AX685729 AX685729 AX685729 AX685729	RESULT 13	2081 AAATGGAAGTG	OY 2021 ATAGTTGTTTTCAAAATAAGGGATCATCTCATTAGCAGGTAGTGAAAGCCATGGCTGGGA 2080	1922	OY 1961 AGATTCACAATGAACTTTCTGATTTTGTATTCAGTTTATTCCAGCTCTTGTCATCCTAGGA 2020	1862 ATGTGTTCCATGACCCAAGGGGATCCAATTCATTGAGAAAAACCTGCCCAGGGGCCACGTCC	1901	QY 1841 GAGTTCTACGGACTGAATTTCACTTGTGGCAGCTCAAATGTTTCTGTGACAACTAATCCA 1900 IIIIIIII			
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Patent: WO 0227016-A 48 04-APR-2002;
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
Shallendra B. (US); Dean, Michael (US)
Location/Qualifiers
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                                                                                           and
                                 (US) ;
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533 c 537 g 484 t Score 1363; DB Pred. No. 3.5e-0; Mismatches 537 g ; DB 6; 3.5e-286; hes 385; щ Length

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CGCCATCTCTGGGAGGCTGCGGCGCACAGGGACCTTGGAAGGGGAAGTGTTTGTGAACGG CGCCATGTCCGGGAGGCTGGGGGCGCGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGG GAGTGGCCAGACCATGTGCATCTTAGGTAGCTCAGGCTCAGGGAAAACCACGCTGCTGGA GAGCGGGCAGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGA

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THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
Shailendra B. (US) ; Dean, Michael (US)
                                                                                        CTGCGCCGGGAGCAGTTCCAGGACTGCTTCTCCTACGTCCTGCAGAGCGACACCCTGCTG
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1/24 GUGGGGTGCTTGGATTCCTGGATTCCTGAAAAGAAAATGCCCATTCCTTT 1783 1621 TCTGGGCTGCTTATTGGATCTGGATTCAGAAACATACAAGAAATGCCCATTCCTTTA 1680 1784 AAAATCATCAGTTATTTACATTCACATACAAAATATTGCAGAATTCTTGTAGTCAATGAG 1843 1681 AAAATCATCAGTTATTTTACATTCCAAAAATATTTGCAGAATTCTTGTAGTCAATGAG 1740 1844 TTCTACGGACTGAATTTCACTTGTGGCAGCTCAAATGATTCTCGTGGTCAATGAG 1740 1844 TTCTACGGACTGAATTTCACTTGTGGCAGCTCAAATGTTTCTGTGGACAACTAATCCAATG 1903 11	1861 TTCACGGCAAACTTCCTCATCTTATATGGGTTTATCCCAGCTCTGGTCATCCTAG 1915
1/24 GUGGGGTGCTTGGATTCCTGAGAAACAGAAATGCCCATTC	1964 TTCACAATGAACTTTCTGA
1/2 GUGGGGTGCTTGGATTCCTGAGAACAAGAAATACAGCCCATTCL	1801 TGCGCCATCACCCAAGGGG
1/2 GUGGGGTGTTGTTGGATTCTCGAGAACAGAAATGACCCATTCL	1904 TGTGCCTTCACTCAAGGAA
1/24 GUGGGGGTGCTTGTTGGATTCCTCGAGAACAAGAATGCCCATTCCTCTGAGAACAAGAATGCCCATTCCTCTGAGAACAAGAATGCCCCATTCCTGTTGTTGTTGTTGTTGTTGTTATCAGAACATACAAGAATGCCCATTCCTGGATTATCAGAAACATACAAGAATGCCCATTCCT784 AAAATCATCAGATTTTACATTCCAAAAATATTGCAGTGAGATTCTTGTAGTCAAAAATATTGCAGTGAGAATTCTTGTAGTCAAAAAATAATGTTTGTAGAGAATTCTGTTGTCAAAAAAATATTGCAGATTCTGTTGTCAAAAAAAA	1741 TTTTACGGCCTGAACTTCA
1/2 GCGGGGTGCTTGTTGGATTCTGGATTCTCGAGAAACAGAAATGCCCATTCL	1844 TTCTACGGACTGAATTTCA
1/24 GCGGGGTGCTTGTTGGATTCCTCAGAAACAAGAATACCCCATTC	
1/24 GCGGGGTGTTGTTGGATCTGGATCCTCAGAAACATACAAGAAATGCCCATTC 	1784 AAAATCATCAGTTATTTTA
1/24 GCGGGGGTGCTTGGTTGGATCTGGATTCCTCAGAAACATACAAGAAATGCCCATTC	1621 TCTGGGCTGCTTATTGGAT
	1724 GCGGGGGTGCTTGTTGGAT

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4 US-09-252-991A-9848

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EARLIER APPLICATION UNMBER: US/09/245,808

CURRENT APPLICATION UNMBER: US/09/245,808

CURRENT FILING DATE: 1998-02-05

EARLIER APPLICATION NUMBER: 05/073763

EARLIER FILING DATE: 1998-02-05

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US-08-314-083B-1

US-08-315-675B-1

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CURRENT APPLICATION NUMBER: US/09/172,108
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL PROGRAM
SEQ ID NO 8
LENGTH: 235
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
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Best Local Similarity 68.9
Conservative
                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                    Sequence 918, Application US/09620312D Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cunnigham, Mary Jane
APPLICANT: Zweiger, Gary B.
APPLICANT: Panzer, Scott R.
APPLICANT: Seilhamer, Jeffrey J.
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                                                                                   APPLICANT:
                                                                                                     APPLICANT:
        APPLICANT:
                                              APPLICANT:
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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                                                                                                                                                                                                                                                                                                                                                                                                           TTACAGGCTCAGAGGCTCGGCACAGCTTAGGTGTCCTGAATGTGTCCTTCAGCGTCAG-A
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                      Xue, Aidong J
                                                                                                                                                          Liu, Chenghua
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    Yonghong
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Pred. No. 3.8e-17;
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RESULT 4
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; NAME/KEY: CDS
; LOCATION: (1)..(2808)
US-09-620-312D-918
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Best Local Similarity 49.6%;
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PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
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APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
TITLE OF INVENTION: No. 6569662el Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/552,317 PRIOR FILING DATE: 2000-04-25
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TYPE: DNA
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                                                                                     CCATTCACCAGCCCCGTTCTGAGCTTTTTCAGCTCTTTGACAA 891
                                                                                                                           GTTTCCAAGTGGTGTCCCTCATGAAGTCCCTGGCACAGGGGGGCCGTACCATCATCTGCA
                                                                                                                                                                                                      TCAACAACCCGCCTGTCATGTTCTTTGATGAGCCCACCAGTGGTCTGGATAGCGCCTCTT
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Zhou, Ping
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Pred. No. 9.6e-13;
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Gaps

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403 668 309

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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, F
APPLICANT: WHITE, Owen
APPLICANT: FRASER, Clai
APPLICANT: VENTER, John
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13705
SEQ ID NO 13705
LENGTH: 1668
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US-09-252-991A-13705
                                                                                                                                         Sequence 2, Application US/09103840A Patent No. 6294328
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            APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 238;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPE
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6551795
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                                                                                                                                                                                                                                                                      ATCAGATTGTCGTCCTCCTGGTGGAACTGGCTCGCAGGAAC 832
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                                                                                                     Robert D.
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Pred. No. 1.1e-05;
                           FOR STRAIN ANALYSIS IN MYCOBACTERIUM
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                                                                                                                                                         Sequence 1, Application US/09103840A Patent No. 6294328
                APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                       APPLICANT: FLEISCHMAN, Robert
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: OTHER INFORMATION: CDC 1551
: OTHER INFORMATION: "n" bases at
: OTHER INFORMATION: represent a,
US-09-103-840A-2
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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2880005 CCGCTCGCTAGCGCAGGGCGACCGTGTGGTGGTGGTCGCGACCCACGACAGCCG 2880058
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Pred. No. 0.0009;
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                                                                        GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FELLING NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
           PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9848
                                                                                                                                                                                                                      Sequence 9848, Application US/09252991A Patent No. 6551795
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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TYPE: DNA
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RESULT 8
US-09-252-991A-9760
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                                         SEQ ID NO 9760
LENGTH: 1713
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     Sequence 9760, Application US/09252991A Patent No. 6551795
                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID.AND AMINO ACID SEQUENCES RELATING TO PSEUDOMON.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                NUMBER OF SEQ ID NOS:
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Best Local Similarity
ORGANISM: Pseudomonas aeruginosa
                          TYPE: DNA
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ORGANISM: Pseudomonas aeruginosa
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Pred. No. 1.3e-05;
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RESULT 9
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                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 10208
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TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
-09-252-991A-10208
                                                                                               PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                     Seguence 10208, Application US/09252991A Patent No. 6551795
                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                         LENGTH: 2805
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Pred. No. 1.8e-05;
0; Mismatches 323;
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                                                                                                                         SEQ ID NO 13436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13436, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60/094,190 PRIOR FILING DATE: US 60
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                        NUMBER OF SEQ ID NOS:
   LENGTH: 1509
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 45.6%;
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Query Match
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15851
ENGTH: 840
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR ADDITORMORE: 1999-02-18
                                                                                                                                                                      Matches
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                           GCAAGTCGACCCTGCTGGCGGCATTGTCGCGCCCTGTTGGCGCCCGGCCGAGGGCCCGGGTGG
                                                        GGAAAACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCGCGCGGGGACCTTCCTGG
                                                                                            ATCTCTCGCTGGCCATCCCCGAGGGTTCGTTCAGTGTGATCGTCGGGCCCAACGCCTGCG
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Pred. No. 4.4e-05;
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US-09-252-991A-13657
; Sequence 13657, App
; Patent No. 6551795
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13657
LENGTH: 2175
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MATC J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
                                                                                                                                                                                                                         299 ACCAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATC
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                                                  GCGCAGGCGGACGCCTGCTGCTGGACGACGTCAGCCTGACCCAGATCGACCCGGCCGAC
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Pred. No. 8.3e-05
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US-09-252-991A-13575
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US-09-252-991A-13575
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NUMBER OF SEQ ID NOS:
SEQ ID NO 13575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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APPLICATION NUMBER: US 60/094,190
FILING DATE: 1998-07-27
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                                                                CGCGAGACGCTGCACTACACCGCGCGCTGCTGGCCATCCGGCGCGCAATCCCGGCTCCTTC
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nilarity 45.3%;
Conservative
                                  -CTGCGCGACAACCTCAACCTGGAGAACGCCGCGCTGGGCGACGACGAACTGCTG
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Pred. No. 8.6e-05
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SEQ ID NO 10998
LENGTH: 993
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Best Local
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ORGANISM: Pseudomonas aeruginosa
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ACTACAGCTTGGGGGGCATTTCCACGGGTGAGCGCGGGGCGCGGGTCTCCATCGCAGCCCAGC
                                                                                 AGGTGGAGGCCGTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGATTGGCA
                                                                                                                  ACGCCGGCAACATCGTGTTCCATGGCGAGGACGTCTCGCAGCACGACGTGC---GCGACC
                                                  AGGCCAAGGTCCACGAGCTG------CTCAACATGGTGCAGCTCGACTGGCTCGCCG
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Sequence 10998, Application US/09252991A
Patent No. 6551795
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CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR ETLING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136 Score 53.4; DB 4; Pred. No. 8e-05; Length 993;

251;

Indels

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PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 10934

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10934
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US-09-252-991A-10934
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Matches 249; Conserv
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GENERAL INFORMATION:
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TITLE OF INVENTION:
FILE REFERENCE: 107
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        492
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                                                                                                                                                            TACGCAAGGAGCTGCGCCGCCTGGCTGGCGCGCCTG 526
                                       CTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTG 820
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                                                                              TGGCGGTGGAGCCGAAGATCCTGCTCCTCGACGAACCCTTCGGCGCCCTCGACGCCAAGG 491
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ilarity 48.3%;
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 9.4e-05;
0; Mismatches 251;
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Search completed: July 27, 2003, 12:45:40 Job time: 165.622 secs